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CUTINASE VARIANTS

FIELD OF THE INVENTION

The present invention relates to a cutinase variant, more particularly to a cutinase variant having improved thermostability. The invention also relates to a DNA sequence encoding the variant, a vector comprising the DNA sequence, a transformed host cell harboring the DNA sequence or the vector, to a method of producing the variant, and to use of the variant.

BACKGROUND OF THE INVENTION

Cutinases are lipolytic enzymes capable of hydrolyzing the substrate cutin. Cutinases are known from various fungi (P.E. Kolattukudy in "Lipases", Ed. B. Borgström and H.L. Brockman, Elsevier 1984, 471-504). The amino acid sequence and the crystal structure of a cutinase of *Fusarium solani pisi* have been described (S. Longhi et al., Journal of Molecular Biology, 268 (4), 779-799 (1997)). The amino acid sequence of a cutinase from *Humicola insolens* has also been published (US 5,827,719).

A number of variants of the cutinase of *Fusarium solani pisi* have been published: WO 94/14963; WO 94/14964; Appl. Environm. Microbiol. 64, 2794-2799, 1998; Proteins: Structure, Function and Genetics 26, 442-458, 1996; J. of Computational Chemistry 17, 1783-1803, 1996; Protein Engineering 6, 157-165, 1993; Proteins: Structure, Function, and Genetics 33, 253-264, 1998.

Fungal cutinases may be used in the enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers (WO 97/27237). However, it is desirable to improve the thermostability of known fungal cutinases to allow a higher process temperature.

SUMMARY OF THE INVENTION

The inventors have found certain variants of fungal cutinases having improved thermostability.

Accordingly, the invention provides a variant of a parent fungal cutinase comprising substitution of one or more amino acid residues which is located:

a) within 17 Å from the location of the N-terminal amino acid (as calculated from amino acid residues in a crystal structure), and/or

b) within 20 positions from the N-terminal amino acid.

The invention also provides a DNA sequence encoding the variant, an expression vector comprising the DNA sequence, a transformed host cell harboring the DNA sequence or the expression vector, and a method of producing the variant by cultivating the transformed host cell so as to produce the variant and recovering the variant from the resulting broth. The invention also provides a process for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate) by treatment with the cutinase variant and a detergent composition comprising the variant.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 shows the 3D structure of the cutinase of *H. insolens*.

Fig. 2 is a computer model showing the three-dimensional structures of the cutinases from *F. solani pisi* (left) and *H. insolens* (right). Different colors have been used to identify the N-terminal amino acid and zones of 12 Å and 17 Å diameter around this.

Figs. 3-6 illustrate the hydrolysis of c3ET. Details are given in the Examples.

DETAILED DESCRIPTION OF THE INVENTION

Fungal cutinase

The parent cutinase is a fungal cutinase, particularly a filamentous fungal cutinase, preferably native to a strain of *Humicola* or *Fusarium*, more preferably *H. insolens* or *F. solani pisi*, most preferably *H. insolens* strain DSM 1800.

The amino acid sequence of the cutinase of *H. insolens* strain DSM 1800 and the DNA sequence encoding it are shown as SEQ ID NO: 2 and SEQ ID NO: 1 of US 5,827,719. The numbering system used herein for the *H. insolens* cutinase is based on the mature peptide, as shown in said SEQ ID NO: 2.

The amino acid sequence of the cutinase of *F. solani pisi* is shown as the mature peptide in Fig. 1D of WO 94/14964. The numbering system used herein for the *F. solani pisi* cutinase is that used in WO 94/14964; it includes the pro-sequence shown in said Fig. 1D; thus, the mature cutinase is at positions 16-214.

The parent cutinase preferably has an amino acid sequence which is at least 50 % (particularly at least 70 % or at least 80 %) homologous to the cutinase of *H. insolens* strain DSM 1800. Preferably, the parent cutinase is one that can be aligned with the cutinase of *H. insolens* strain DSM 1800.

Homology and alignment

For purposes of the present invention, the degree of homology may be suitably determined according to the method described in Needleman, S.B. and Wunsch, C.D., (1970), Journal of Molecular Biology, 48, 443-45, with the following settings for polypeptide sequence comparison: GAP creation penalty of 3.0 and GAP extension penalty of 0.1. The determination may be done by means of a computer program known such as GAP provided in the GCG program package (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711).

Two given sequences can be aligned according to the method described in Needleman (*supra*) using the same parameters. This may be done by means of the GAP program (*supra*)..

Three-dimensional structure of cutinase

The structure of the cutinase of *H. insolens* was solved in accordance with the principle for X-ray crystallographic methods as given, for example, in X-Ray Structure Determination, Stout, G.K. and Jensen, L.H., John Wiley & Sons, Inc. NY, 1989. The structural coordinates for the solved crystal structure at 2.2 Å resolution using the isomorphous replacement method are given in Fig. 1 in standard PDB format (Protein Data Bank, Brookhaven National Laboratory, Brookhaven, CT).

The structure of the cutinase of *F. solani pisi* is described in Martinez et al. (1992) Nature 356, 615-618. The 3D structures of the cutinases of *F. solani pisi* and *H. insolens* are compared as a computer model in Fig. 2.

It should be noted that the overall three-dimensional structure of the fungal cutinases is very similar and has been shown by X-ray crystallography to be highly homologous. The similarities between the cutinases from *F. solani pisi* and *H. insolens* is clearly apparent from the computer model in Fig. 2. It is therefore to be expected that modifications of the type indicated for one fungal cutinase will also be functional for other fungal cutinases.

Substitution near N-terminal

The variant of the invention has one or more amino acid substitutions in the vicinity of the N-terminal. The substitution is within a distance of 17 Å (preferably within 12 Å) and/or within 20 positions (preferably within 15 positions) of the N-terminal. The distance from the N-terminal is to be calculated between the Cα atom of the amino acids, and is calculated from an amino acid in a crystal structure (i.e. visible in the X-ray structure).

In the cutinase of *H. insolens* strain DSM 1800, the two N-terminal amino acids Q1 and L2 are not visible in the X-ray structure, so the distance is to be calculated from amino acid G3. Amino acids within 17 Å include positions 3-12, 18, 20-60, 62-64, 82, 85-86, 100-108, 110-111, 130-132, 174, 176-182, 184-185, 188, and 192. Those within 12 Å include positions 3-8, 22-27, 30-47, 53-59, 102, 177, and 180-181.

In the cutinase of *F. solani pisi*, the N-terminal amino acid G17 is visible in the X-ray structure. Amino acids within 17 Å include positions 17-26, 34-75, 77-79, 101, 115, 117-119, 147, 191-197, 199-200, and 203. Those within 12 Å include positions 17-22, 38, 40, 45-58, 60, 65, and 70-72.

The variants of the invention have improved thermostability compared to the parent enzyme. The thermostability may be determined from the denaturation temperature by DSC (differential scanning calorimetry), e.g. as described in an example, e.g. at pH 8.5 with a scan rate of 90 K/hr. Preferred variants have a denaturation temperature which is at least 5°C higher than the parent enzyme.

The total number of substitutions in the above regions is typically not more than 10, e.g. not more than substitutions in the above regions. In addition, the cutinase variant of the invention may optionally include other modifications of the parent enzyme, typically not more than 10, e.g. not more than 5 alterations (substitutions,

deletions or insertions) outside of the above regions. Thus, the total amino acid sequence of the variant may have not more than 20, e.g. not more than 10 alterations compared to the parent cutinase.

Solvent accessible surface

One or more of the substitutions is preferably made at an exposed amino acid residue, i.e. an amino acid residue having a solvent accessible surface. This can be calculated by teh "dssp" program (version October 1988) described in W. Kabsch and C. Sander, Biopolymers, 22 (1983) pp. 2577-2637.

In the cutinase of *H. insolens* strain DSM 1800, the following amino acids lie within 17 Å of G3 at the N-terminal and have a solvent accessible surface greater than 0: 3-12, 18, 26-33, 36-38, 40-45, 47-56, 59-60, 62-64, 82, 85-86, 104-105, 174, 176-179, 181-182, 192.

Preferred substitutions

A preferred substitution near the N-terminal is one that increases the electrical charge, i.e. a substitution of a negatively charged amino acid with a neutral or positively charged amino acid or substitution of a neutral amino acid with a positively charged amino acid. This substitution may be made at a position corresponding to position E6, E10, E47 or E179 in the cutinase of *Humicola insolens* strain DSM 1800, preferably a substitution corresponding to E6Q, E10Q, E47K or E179Q.

Another preferred substitution near the N-terminal is substitution with a Pro residue, preferably a substitution corresponding to A14P or R51P in the cutinase of *Humicola insolens* strain DSM 1800.

Preferred variants

The following are some preferred variants in the *H. insolens* cutinase. Corresponding variants of other parent cutinases are also preferred. (JC numbers are the inventors' designations).

JC006: R51P

JC011: E6Q, L138I

JC013: A14P, E47K

JC014, JC015: E47K

JC025: E179Q

JC026: E6Q, E47K, R51P

JC029: A14P, E47K, E179Q

JC030: E47K, E179Q

JC031: E47K, D63N

JC038: E6Q, A14P, E47K, R51P, E179Q

JC039: E6Q, E10Q, A14P, E47K, R51P, E179Q

JC040: Q1P, L2V, S11C, N15T, F24Y, L46I, E47K

Use of cutinase variant

The cutinase variant of the invention may be used, e.g., for the enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), such as cyclic tri(ethylene terephthalate), abbreviated as c3ET.

In particular, this may be used to remove such cyclic oligomers from polyester containing fabric or yarn by treating the fabric or yarn with the cutinase variant, preferably followed by rinsing the fabric or yarn with an aqueous solution having a pH in the range of from about pH 7 to about pH 11. The treatment of polyester is preferably carried out above the glass transition temperature of c3ET (about 55°C) and below the glass transition temperature of polyester (about 70°C). Thus, the treatment is preferably carried out at 55-70°C, e.g. at 60-65°C. The process may be carried out in analogy with WO 97/27237.

The cutinase variant of the invention is also useful in detergents, where it may be incorporated to improve the removal of fatty soiling, as described in WO 94/03578 and WO 94/14964.

Nomenclature for amino acid alterations

The nomenclature used herein for defining mutations is basically as described in WO 92/05249. Thus, R51P indicates substitution of R in position 51 with P.

Methods for preparing cutinase variants

The cutinase variant of the invention can be prepared by methods known in the art, e.g. as described in WO 94/14963 or WO 94/14964 (Unilever). The following describes methods for the cloning of cutinase-encoding DNA sequences, followed by methods for generating mutations at specific sites within the cutinase-encoding sequence.

Cloning a DNA sequence encoding a cutinase

The DNA sequence encoding a parent cutinase may be isolated from any cell or microorganism producing the cutinase in question, using various methods well known in the art. First, a genomic DNA and/or cDNA library should be constructed using chromosomal DNA or messenger RNA from the organism that produces the cutinase to be studied. Then, if the amino acid sequence of the cutinase is known, labeled oligonucleotide probes may be synthesized and used to identify cutinase-encoding clones from a genomic library prepared from the organism in question. Alternatively, a labeled oligonucleotide probe containing sequences homologous to another known cutinase gene could be used as a probe to identify cutinase-encoding clones, using hybridization and washing conditions of lower stringency.

Yet another method for identifying cutinase-encoding clones would involve inserting fragments of genomic DNA into an expression vector, such as a plasmid, transforming cutinase-negative bacteria with the resulting genomic DNA library, and then plating the transformed bacteria onto agar containing a substrate for cutinase (*i.e.* maltose), thereby allowing clones expressing the cutinase to be identified.

Alternatively, the DNA sequence encoding the enzyme may be prepared synthetically by established standard methods, *e.g.* the phosphoroamidite method described S.L. Beaucage and M.H. Caruthers, (1981), Tetrahedron Letters 22, p. 1859-1869, or the method described by Matthes et al., (1984), EMBO J. 3, p. 801-805. In the phosphoroamidite method, oligonucleotides are synthesized, *e.g.* in an automatic DNA synthesizer, purified, annealed, ligated and cloned in appropriate vectors.

Finally, the DNA sequence may be of mixed genomic and synthetic origin, mixed synthetic and cDNA origin or mixed genomic and cDNA origin, prepared by

ligating fragments of synthetic, genomic or cDNA origin (as appropriate, the fragments corresponding to various parts of the entire DNA sequence), in accordance with standard techniques. The DNA sequence may also be prepared by polymerase chain reaction (PCR) using specific primers, for instance as described in US 4,683,202 or R.K. Saiki et al., (1988), Science 239, 1988, pp. 487-491.

Site-directed mutagenesis

Once a cutinase-encoding DNA sequence has been isolated, and desirable sites for mutation identified, mutations may be introduced using synthetic oligonucleotides. These oligonucleotides contain nucleotide sequences flanking the desired mutation sites. In a specific method, a single-stranded gap of DNA, the cutinase-encoding sequence, is created in a vector carrying the cutinase gene. Then the synthetic nucleotide, bearing the desired mutation, is annealed to a homologous portion of the single-stranded DNA. The remaining gap is then filled in with DNA polymerase I (Klenow fragment) and the construct is ligated using T4 ligase. A specific example of this method is described in Morinaga et al., (1984), Biotechnology 2, p. 646-639. US 4,760,025 discloses the introduction of oligonucleotides encoding multiple mutations by performing minor alterations of the cassette. However, an even greater variety of mutations can be introduced at any one time by the Morinaga method, because a multitude of oligonucleotides, of various lengths, can be introduced.

Another method for introducing mutations into cutinase-encoding DNA sequences is described in Nelson and Long, (1989), Analytical Biochemistry 180, p. 147-151. It involves the 3-step generation of a PCR fragment containing the desired mutation introduced by using a chemically synthesized DNA strand as one of the primers in the PCR reactions. From the PCR-generated fragment, a DNA fragment carrying the mutation may be isolated by cleavage with restriction endonucleases and reinserted into an expression plasmid.

Expression of cutinase variants

According to the invention, a DNA sequence encoding the variant produced by methods described above, or by any alternative methods known in the art, can be expressed, in enzyme form, using an expression vector which typically includes con-

trol sequences encoding a promoter, operator, ribosome binding site, translation initiation signal, and, optionally, a repressor gene or various activator genes.

Expression vector

The recombinant expression vector carrying the DNA sequence encoding a cutinase variant of the invention may be any vector which may conveniently be subjected to recombinant DNA procedures, and the choice of vector will often depend on the host cell into which it is to be introduced. The vector may be one which, when introduced into a host cell, is integrated into the host cell genome and replicated together with the chromosome(s) into which it has been integrated. Examples of suitable expression vectors include pMT838.

Promoter

In the vector, the DNA sequence should be operably connected to a suitable promoter sequence. The promoter may be any DNA sequence which shows transcriptional activity in the host cell of choice and may be derived from genes encoding proteins either homologous or heterologous to the host cell.

Examples of suitable promoters for directing the transcription of the DNA sequence encoding a cutinase variant of the invention, especially in a bacterial host, are the promoter of the *lac* operon of *E.coli*, the *Streptomyces coelicolor* agarase gene *dag*A promoters, the promoters of the *Bacillus licheniformis* α-amylase gene (*amyL*), the promoters of the *Bacillus stearothermophilus* maltogenic amylase gene (*amyM*), the promoters of the *Bacillus amyloliquefaciens* α-amylase (*amyQ*), the promoters of the *Bacillus subtilis* xylA and xylB genes etc. For transcription in a fungal host, examples of useful promoters are those derived from the gene encoding *A. oryzae* TAKA amylase, the TPI (triose phosphate isomerase) promoter from *S. cerevisiae* (Alber et al. (1982), J. Mol. Appl. Genet 1, p. 419-434, *Rhizomucor miehei* aspartic proteinase, *A. niger* neutral α-amylase, *A. niger* acid stable α-amylase, *A. niger* glucoamylase, *Rhizomucor miehei* lipase, *A. oryzae* alkaline protease, *A. oryzae* triose phosphate isomerase or *A. nidulans* acetamidase.

Expression vector

The expression vector of the invention may also comprise a suitable transcription terminator and, in eukaryotes, polyadenylation sequences operably connected to the DNA sequence encoding the α-amylase variant of the invention. Termination and polyadenylation sequences may suitably be derived from the same sources as the promoter.

The vector may further comprise a DNA sequence enabling the vector to replicate in the host cell in question. Examples of such sequences are the origins of replication of plasmids pUC19, pACYC177, pUB110, pE194, pAMB1 and pIJ702.

The vector may also comprise a selectable marker, e.g. a gene the product of which complements a defect in the host cell, such as the *dal* genes from *B. subtilis* or *B. licheniformis*, or one which confers antibiotic resistance such as ampicillin, kanamycin, chloramphenicol or tetracyclin resistance. Furthermore, the vector may comprise *Aspergillus* selection markers such as amdS, argB, niaD and sC, a marker giving rise to hygromycin resistance, or the selection may be accomplished by co-transformation, *e.g.* as described in WO 91/17243.

The procedures used to ligate the DNA construct of the invention encoding a cutinase variant, the promoter, terminator and other elements, respectively, and to insert them into suitable vectors containing the information necessary for replication, are well known to persons skilled in the art (cf., for instance, Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor, 1989).

Host Cells

The cell of the invention, either comprising a DNA construct or an expression vector of the invention as defined above, is advantageously used as a host cell in the recombinant production of a cutinase variant of the invention. The cell may be transformed with the DNA construct of the invention encoding the variant, conveniently by integrating the DNA construct (in one or more copies) in the host chromosome. This integration is generally considered to be an advantage as the DNA sequence is more likely to be stably maintained in the cell. Integration of the DNA constructs into the host chromosome may be performed according to conventional methods, *e.g.* by ho-

mologous or heterologous recombination. Alternatively, the cell may be transformed with an expression vector as described above in connection with the different types of host cells.

The cell of the invention may be a cell of a higher organism such as a mammal or an insect, but is preferably a microbial cell, e.g. a bacterial or a fungal (including yeast) cell.

Examples of suitable bacteria are Gram positive bacteria such as *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus lautus*, *Bacillus megaterium*, *Bacillus thuringiensis*, or *Streptomyces lividans* or *Streptomyces murinus*, or gramnegative bacteria such as *E.coli*. The transformation of the bacteria may, for instance, be effected by protoplast transformation or by using competent cells in a manner known *per se*.

The yeast organism may favorably be selected from a species of *Saccharomyces* or *Schizosaccharomyces*, *e.g. Saccharomyces cerevisiae*.

The host cell may also be a filamentous fungus *e.g.* a strain belonging to a species of *Aspergillus*, most preferably *Aspergillus oryzae* or *Aspergillus niger*, or a strain of *Fusarium*, such as a strain of *Fusarium oxysporium*, *Fusarium graminearum* (in the perfect state named *Gribberella zeae*, previously *Sphaeria zeae*, *synonym with Gibberella roseum and Gibberella roseum* f. sp. *cerealis)*, or *Fusarium sulphureum* (in the prefect state named *Gibberella puricaris*, synonym with *Fusarium trichothecioides*, *Fusarium bactridioides*, *Fusarium sambucium*, *Fusarium roseum*, and *Fusarium roseum var. graminearum)*, *Fusarium cerealis* (synonym with *Fusarium crokkwellnse*), or *Fusarium venenatum*.

In a preferred embodiment of the invention the host cell is a protease deficient or protease minus strain.

This may for instance be the protease deficient strain *Aspergillus oryzae* JaL 125 having the alkaline protease gene named "alp" deleted. This strain is described in WO 97/35956 (Novo Nordisk).

Filamentous fungi cells may be transformed by a process involving protoplast formation and transformation of the protoplasts followed by regeneration of the cell wall in a manner known per se. The use of *Aspergillus* as a host micro-organism is de-

scribed in EP 238 023 (Novo Nordisk A/S), the contents of which are hereby incorporated by reference.

Method of producing the cutinase variant of the invention

In yet a further aspect, the present invention relates to a method of producing a cutinase variant of the invention, which method comprises cultivating a host cell under conditions conducive to the production of the variant and recovering the variant from the cells and/or culture medium.

The medium used to cultivate the cells may be any conventional medium suitable for growing the host cell in question and obtaining expression of the cutinase variant of the invention. Suitable media are available from commercial suppliers or may be prepared according to published recipes (*e.g.* as described in catalogues of the American Type Culture Collection).

The cutinase variant secreted from the host cells may conveniently be recovered from the culture medium by well-known procedures, including separating the cells from the medium by centrifugation or filtration, and precipitating proteinaceous components of the medium by means of a salt such as ammonium sulphate, followed by the use of chromatographic procedures such as ion exchange chromatography, affinity chromatography, or the like.

Expression of variant in plants

The present invention also relates to a transgenic plant, plant part or plant cell which has been transformed with a DNA sequence encoding the variant of the invention so as to express and produce this enzyme in recoverable quantities. The enzyme may be recovered from the plant or plant part. Alternatively, the plant or plant part containing the recombinant enzyme may be used as such.

The transgenic plant can be dicotyledonous or monocotyledonous, for short a dicot or a monocot. Examples of monocot plants are grasses, such as meadow grass (blue grass, Poa), forage grass such as festuca, lolium, temperate grass, such as Agrostis, and cereals, e.g. wheat, oats, rye, barley, rice, sorghum and maize (corn).

Examples of dicot plants are tobacco, legumes, such as lupins, potato, sugar beet, pea, bean and soybean, and cruciferous (family Brassicaceae), such as cauliflower, oil seed rape and the closely related model organism Arabidopsis thaliana.

Examples of plant parts are stem, callus, leaves, root, fruits, seeds, and tubers. In the present context, also specific plant tissues, such as chloroplast, apoplast, mitochondria, vacuole, peroxisomes and cytoplasm are considered to be a plant part. Furthermore, any plant cell, whatever the tissue origin, is considered to be a plant part.

Also included within the scope of the invention are the progeny of such plants, plant parts and plant cells.

The transgenic plant or plant cell expressing the variant of the invention may be constructed in accordance with methods known in the art. In short the plant or plant cell is constructed by incorporating one or more expression constructs encoding the enzyme of the invention into the plant host genome and propagating the resulting modified plant or plant cell into a transgenic plant or plant cell.

Conveniently, the expression construct is a DNA construct which comprises a gene encoding the enzyme of the invention in operable association with appropriate regulatory sequences required for expression of the gene in the plant or plant part of choice. Furthermore, the expression construct may comprise a selectable marker useful for identifying host cells into which the expression construct has been integrated and DNA sequences necessary for introduction of the construct into the plant in question (the latter depends on the DNA introduction method to be used).

The choice of regulatory sequences, such as promoter and terminator sequences and optionally signal or transit sequences is determined, eg on the basis of when, where and how the enzyme is desired to be expressed. For instance, the expression of the gene encoding the enzyme of the invention may be constitutive or inducible, or may be developmental, stage or tissue specific, and the gene product may be targeted to a specific tissue or plant part such as seeds or leaves. Regulatory sequences are eg described by Tague et al, Plant, Phys., 86, 506, 1988.

For constitutive expression the 35S-CaMV promoter may be used (Franck et al., 1980. Cell 21: 285-294). Organ-specific promoters may eg be a promoter from

storage sink tissues such as seeds, potato tubers, and fruits (Edwards & Coruzzi, 1990. Annu. Rev. Genet. 24: 275-303), or from metabolic sink tissues such as meristems (Ito et al., 1994. Plant Mol. Biol. 24: 863-878), a seed specific promoter such as the glutelin, prolamin, globulin or albumin promoter from rice (Wu et al., Plant and Cell Physiology Vol. 39, No. 8 pp. 885-889 (1998)), a *Vicia faba* promoter from the legumin B4 and the unknown seed protein gene from *Vicia faba* described by Conrad U. et al, Journal of Plant Physiology Vol. 152, No. 6 pp. 708-711 (1998), a promotter from a seed oil body protein (Chen et al., Plant and cell physiology vol. 39, No. 9 pp. 935-941 (1998), the storage protein napA promoter from Brassica napus, or any other seed specific promoter known in the art, eg as described in WO 91/14772. Furthermore, the promoter may be a leaf specific promoter such as the rbcs promoter from rice or tomato (Kyozuka et al., Plant Physiology Vol. 102, No. 3 pp. 991-1000 (1993), the chlorella virus adenine methyltransferase gene promoter (Mitra, A. and Higgins, DW, Plant Molecular Biology Vol. 26, No. 1 pp. 85-93 (1994), or the aldP gene promoter from rice (Kagaya et al., Molecular and General Genetics Vol. 248, No. 6 pp. 668-674 (1995), or a wound inducible promoter such as the potato pin2 promoter (Xu et al, Plant Molecular Biology Vol. 22, No. 4 pp. 573-588 (1993).

A promoter enhancer element may be used to achieve higher expression of the enzyme in the plant. For instance, the promoter enhancer element may be an intron which is placed between the promoter and the nucleotide sequence encoding the enzyme. For instance, Xu et al. *op cit* disclose the use of the first intron of the rice actin 1 gene to enhance expression.

The selectable marker gene and any other parts of the expression construct may be chosen from those available in the art.

The DNA construct is incorporated into the plant genome according to conventional techniques known in the art, including *Agrobacterium*-mediated transformation, virus-mediated transformation, micro injection, particle bombardment, biolistic transformation, and electroporation (Gasser et al, Science, 244, 1293; Potrykus, Bio/Techn. 8, 535, 1990; Shimamoto et al, Nature, 338, 274, 1989).

Presently, *Agrobacterium tumefaciens* mediated gene transfer is the method of choice for generating transgenic dicots (for review Hooykas & Schilperoort, 1992. Plant Mol. Biol. 19: 15-38), however it can also be used for transforming monocots,

although other transformation methods are generally preferred for these plants. Presently, the method of choice for generating transgenic monocots is particle bombardment (microscopic gold or tungsten particles coated with the transforming DNA) of embryonic calli or developing embryos (Christou, 1992. Plant J. 2: 275-281; Shimamoto, 1994. Curr. Opin. Biotechnol. 5: 158-162; Vasil et al., 1992. Bio/Technology 10: 667-674). An alternative method for transformation of monocots is based on protoplast transformation as described by Omirulleh S, et al., Plant Molecular biology Vol. 21, No. 3 pp. 415-428 (1993).

Following transformation, the transformants having incorporated the expression construct are selected and regenerated into whole plants according to methods well-known in the art.

MATERIALS AND METHODS

Plasmids

pJSO026

This is a *S. cerevisiae* expression plasmid described in WO 97/07205 and in J.S.Okkels, (1996) "A URA3-promoter deletion in a pYES vector increases the expression level of a fungal lipase in Saccharomyces cerevisiae. Recombinant DNA Biotechnology III: The Integration of Biological and Engineering Sciences, vol. 782 of the Annals of the New York Academy of Sciences).

pFuku83

This is a yeast and E. coli shuttle vector for expression of the H. insolens cutinase under the control of a TPI promoter, constructed from pJSO026.

Substrate

BETEB

Terephthalic acid bis(2-hydroxyethyl)ester dibenzoate is herein abbreviated as BETEB (benzoyl-ethylene-terephthalic-ethelene-benzoate). It was prepared from terephthalic acid bis (2-hydroxyethyl) ester and benzoic acid.

Lipase activity (LU)

A substrate for lipase is prepared by emulsifying tributyrin (glycerin tributyrate) using gum Arabic as emulsifier. The hydrolysis of tributyrin at 30 °C at pH 7 is followed in a pH-stat titration experiment. One unit of lipase activity (1 LU) equals the amount of enzyme capable of releasing 1 µmol butyric acid/min at the standard conditions.

Differential scanning calorimetry (DSC)

Sample and reference solutions are carefully degassed immediately prior to loading of samples into the calorimeter (reference: buffer without enzyme). Sample and reference solutions (approx. 0.5 ml) are thermally pre-equillibrated for 20 minutes at 5°C. The DSC scan is performed from 5 C to 95 C at a scan rate of approx. 90 K/hr. Denaturation temperatures are determined at an accuracy of approx. +/- 1 C. A VP-DSC from MicroCal Inc. is suitable for the experiments.

Methods

PCR conditions

step 1: 94° C, 120 sec.

step 2: 94° C, 60 sec

step 3: 50° C, 60 sec

step 4: 72° C, 150 sec.

Go to step 2, 35 cycles

step 5: 72° C, 480 sec.

Step 6: 4° C, for ever

EXAMPLES

Example 1

Preparation of cutinase variants

A DNA sequence encoding *H. insolens* cutinase was obtained as described in US 5,827,719 (Novo Nordisk) and was found to have the DNA sequence shown in SEQ ID NO: 1 therein.

Variants were prepared by localized random mutagenesis and selection of positive clones by incubation at 60°C for 1 day on BETEB plates. The BETEB plates contained 200 ml/l of 500 mM glycine buffer (pH 8.5), 1.25 g/l of BETEB (dissolved in hot ethanol) and 20 g/l of agar.

Three positive variants (denoted JC013, JC014, JC025) were isolated, and their amino acid sequence was determined. They were found to have the following modifications, compared to the parent *H. insolens* cutinase:

JC013: A14P + E47K

JC014: E47K

JC025: E179Q

Example 2

Site directed mutation

JC026 (E6Q, E47K, R51P) was prepared as follows:

A pair of PCR primers were designed so as to introduce amino acid substitutions, making use of the existed restriction enzyme sites nearby, as follows (an asterisk indicates an introduced mutation):

Upper primer: E6Q F

cgg cag ctg gga gcc atc c*ag aac

Pvu II

Lower primer: E47K,R51P

cgc cct gga tcc aga tgt tcg* gga tgt ggg act t*aa ggc

*Bam*H I

PCR was run using these primers and pFukuNL83 as a template under the PCR condition described above.

The obtained PCR fragment was purified by Clontech Spincolumn and digested with *Pvu* II and *Bam*H I.

The resultant fragment was gel-purified and ligated to pFukuNL83 which had been digested with the same restriction enzyme sites.

Example 3

Thermostability of cutinase variants

Thermostability of cutinase variants was investigated by means of DSC (Differential Scanning Calorimetry) at pH 4.5 (50 mM acetate buffer) and pH 8.5 (50mM glycyl-glycine buffer). The thermal denaturation temperature, Td, was taken as the top of denaturation peak (major endothermic peak) in thermograms (Cp vs. T) obtained after heating of enzyme solutions at a constant programmed heating rate. The parent cutinase (NL83) was included for comparison. Results:

	pH 4.5	pH 8.5
JC013	-	70
JC014	-	70
JC015	65	70
JC026	64	71
JC029	66	73
JC038	64	71
JC039	66	73
NL83 (parent)	61	63

The results show improved thermostability in all cases. The improvement is seen to be 3-5° at pH 4.5, and 7-10° at pH 8.5.

Example 4

Hydrolysis of BETEB

The thermostability of *H, insolens* cutinase variants JC014 (E47K) and JC025 (E179Q) was measured by hydrolysis of BETEB at elevated temperature. The parent

cutinase (denoted NL83) was tested for comparison. For each cutinase, the following mixture was incubated for 17 hours at various temperatures in the range 55-70°C::

0.1 ml 0.5 M glycyl-glycine buffer (pH 8.5)
0.1 ml 0.5 % BETEB dissolved in ethanol
0.1 ml enzyme solution (approx. 25 LU/ml)
0.7 ml Milli Q water

The degree of hydrolysis was measured after the incubation. The results are shown in the table below.

	JC014	JC025	NL83 (parent)
55°C	27 LU/ml	25 LU/ml	24 LU/ml
60°C	98 %	99 %	72 %
65°C	91 %	83 %	33 %
70°C	66 %	13 %	7 %
	6 %	6 %	7 %

These results clearly show that the variants have improved thermostability compared to the parent cutinase.

Example 5

Hydrolysis of BETEB

The thermostability of cutinase variants JC013, JC038 and JC039 was measured by hydrolysis of BETEB at 60°C for 2 hours. The parent cutinase (denoted NL83) was tested for comparison. The hydrolysis was carried out at the same conditions as in Example 2, except that the temperature was fixed at 60°C and the cutinase dosage was varied. The results below are shown in the table below.

LU/ml	JC038	JC039	JC013	NL83 (parent)
0	0 %	0 %	0 %	0 %
10	97 %	99 %	9 %	6 %
20	98 %	99 %	74 %	
50	98 %	94 %	93 %	15 %
100	88 %	69 %	92 %	34 %

300	41 %
600	63 %
1200	82 %

The results show a much faster hydrolysis at 60°C with the variants than with the parent cutinase.

Example 6

Hydrolysis of c3ET

The thermostability of variants was measured by hydrolysis of c3ET at elevated temperature. Wild type (NL83) was tested for comparison. For each cutinase, the following mixture was incubated for 2 hours at various temperatures.

0.115mg c3ET (0.1ml of 2mM c3ET dissolved in HFIP was taken in reaction vessel. Solvent was removed under vacuum, then dried up at 70°C over night)

0.1ml 0.5M glycyl-glycine buffer (pH8.5)

0.1ml enzyme solution (approx. 600LU/ml)

0.8ml Milli Q water

After the incubation, 2ml of 1,1,1,3,3,3-Hexafluoro-2-propanol (HFIP) was added to each reaction mixture, then hydrolysis ratio was measured by HPLC. The results shown in Fig 3 clearly indicate the variants especially JC039 have improved thermostability compared to the parent cutinase.

Example 7

Hydrolysis of c3ET on yarn

Similar experiment to the previous example was done using polyester yarn containing c3ET as by product. The following substrate mixture was preincubated at 60 or 65°C:

0.1g polyester yarn

0.2ml 0.5M glycyl-glycine buffer (pH8.5)

1.7ml Milli Q water

After preincubation, 0.1ml enzyme solution (approx. 1000 LU/ml) was added to each reaction vessel and incubated for 17 hours. Then 2ml HFIP was added and

left for 30 minutes to extract and hydrolyze c3ET sitting on the surface of the polyester yarn; then the hydrolysis ratio was measured. The results are shown in Fig. 4.

It is seen that the variants are more effective than the parent cutinase for hydrolyzing c3ET on polyester yarn, particularly JC039. It is also seen that JC039 gives higher hydrolysis ratio at 65°C than 60°C.

Example 8

Treatment of yarn by variant JC039

Time courses of c3ET hydrolysis on polyester yarn at different temperature or dosage were examined. Time course at different temperatures is shown in Fig 5. It is seen that optimal temperature of JC039 is 65°C. At 70°C there is still about half of the activity left. Time course with increased enzyme dosage is shown in Fig 6. The curves at dosage 275 and 550 LU/ml are seen to be the same, indicating that the hydrolysis ratio reached to plateau between dosage of 100 to 275 LU/ml. Presumably 200LU/ml is enough.

CLAIMS

1. A variant of a parent fungal cutinase, which variant:
   a) comprises substitution of one or more amino acid residues at a position which is located:
      i) within 17 Å from the location of the N-terminal amino acid (as calculated from amino acid residues in a crystal structure), and/or
      ii) within 20 positions from the N-terminal amino acid, and
   b) is more thermostable than the parent cutinase.

2. The variant of the preceding claim which comprises substitution of one or more amino acid residues at a position which is located:
      i) within 12 Å from the location of the N-terminal amino acid (as calculated from amino acid residues in a crystal structure), and/or
      ii) within 15 positions from the N-terminal amino acid.

3. A variant of a parent fungal cutinase comprising substitution of one or more amino acid residues which is located:
   a) within 17 Å from the location of the N-terminal amino acid (as calculated from amino acid residues in a crystal structure), and/or
   b) within 20 positions from the N-terminal amino acid,

   with the proviso that it is not a variant of the cutinase of *Fusarium solani pisi* having one of the substitutions R17, T18, T19V, D21N, I24E, Y38F, R40, G41A, S42, T43, E44, T45, G46, N47R, G49, T50, L51, P53, S54, A56C, S57, N58R, S61, A62E, K65A, D66S, G67D, W69Y, I70C, G74, G75, R78, Y119, G192, P193, D194R, A195, R196, G197V, or A199C (*Fusarium solani pisi* cutinase numbering).

4. A variant of a parent fungal cutinase comprising substitution of one or more amino acid residues which:
   a) has a solvent accessible surface, and
   b) is located:

i) within 17 Å from the location of the N-terminal amino acid (as calculated from amino acid residues in a crystal structure), and/or

ii) within 20 positions from the N-terminal amino acid,

with the proviso that it is not a variant of the cutinase of *Fusarium solani pisi* having one of the substitutions T18, Y38F, R40, G41A, S42, T43, E44, T45, N47R, G49, T50, L51, P53, S54, A56C, A62E or G192 (*Fusarium solani pisi* cutinase numbering).

5. A variant of a parent fungal cutinase comprising substitution of one or more amino acid residues which is located:

a) less than 12 Å from the location of the N-terminal amino group (as calculated from amino acid residues in a crystal structure), and/or

b) within 15 positions from the N-terminal amino acid,

with the proviso that the variant is not the cutinase of *Fusarium solani pisi* having one of the substitutions R17, T18, T19V, D21N, Y38F, R40, T45, G46, N47R, G49, T50, L51, P53, S54, A56C, S57, N58R, K65A or I70C (*Fusarium solani pisi* cutinase numbering).

6. The variant of any preceding claim wherein the parent cutinase is native to a filamentous fungus, preferably a strain of *Humicola* or *Fusarium*, preferably *H. insolens* or *F. solani pisi*, most preferably *H. insolens* strain DSM 1800.

7. The variant of any preceding claim wherein the parent cutinase has an amino acid sequence which can be aligned with the cutinase of *H. insolens* strain DSM 1800.

8. The variant of any preceding claim wherein the parent cutinase has an amino acid sequence which is at least 50 % homologous to the cutinase of *H. insolens* strain DSM 1800, preferably at least 70 % homologous, more preferably at least 80 % homologous.

9. A variant of a parent fungal cutinase from *Humicola insolens* which comprises substitution of one or more amino acid residues located:

a) within 17 Å from the location of the N-terminal amino acid (as calculated from amino acid residues in a crystal structure), and/or

b) within 20 positions from the N-terminal amino acid.

10. The variant of the preceding claim which comprises substitution of one or more amino acid residues located:

a) less than 12 Å from the location of the N-terminal amino group (as calculated from amino acid residues in a crystal structure), and/or

b) within 15 positions from the N-terminal amino acid

11. The variant of any preceding claim which comprises substitution of one or more amino acids having a solvent accessible surface.

12. The variant of any preceding claim wherein one or more substitutions is substitution of a negatively charged amino acid with a neutral or positively charged amino acid or substitution of a neutral amino acid with a positively charged amino acid.

13. The variant of any preceding claim wherein one or more substitutions is substitution with a Pro residue.

14. The variant of any preceding claim wherein one or more substitutions is at a position corresponding to position E6, E10, A14, E47, R51 and/or E179 in the cutinase of *Humicola insolens* strain DSM 1800, preferably a substitution corresponding to E6Q, E10Q, A14P, E47K, R51P and/or E179Q (*H. insolens* cutinase numbering).

15. The variant of any preceding claim which has one, two, three, four , five or six of said substitutions.

16. The variant of any preceding claim which has substitutions corresponding to one of the following in the cutinase of *Humicola insolens* strain DSM 1800:

a) R51P

b) E6Q, L138I

c) A14P, E47K
d) E47K
e) E179Q
f) E6Q, E47K, R51P
g) A14P, E47K, E179Q
h) E47K, E179Q
i) E47K, D63N
j) E6Q, A14P, E47K, R51P, E179Q
k) E6Q, E10Q, A14P, E47K, R51P, E179Q, or
l) Q1P, L2V, S11C, N15T, F24Y, L46I, E47K

17. The variant of any preceding claim which has hydrolytic activity towards terephthalic acid esters, particularly towards cyclic tri(ethylene terephthalate) and/or Terephthalic acid bis(2-hydroxyethyl)ester dibenzoate (BETEB).

18. The variant of any preceding claim which has a denaturation temperature which is at least 5° higher than the parent cutinase, preferably measured at pH 8.5

19. A DNA sequence encoding the variant of any preceding claim.

20. A vector comprising the DNA sequence of the preceding claim.

21. A transformed host cell harboring the DNA sequence of claim 19 or the vector of claim 20.

22. A method of producing the variant of any of claims 1-18 comprising
a) cultivating the cell of claim 21 so as to express and preferably secrete the variant, and
b) recovering the variant.

23. A method of constructing a cutinase variant, which method comprises:
a) selecting a parent fungal cutinase,

b) identifying one or more amino acid residues in the parent cutinase at positions which are:

i) within 17 Å from the location of the N-terminal amino acid (as calculated from amino acid residues in a crystal structure), and/or

ii) within 20 positions from the N-terminal amino acid, and

c) making alterations each of which is an insertion, a deletion or a substitution of the amino acid residue,

d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b),

e) preparing the variant resulting from steps b-d,

f) testing the thermostability of the variant,

g) optionally repeating steps b-f, and

h) selecting a variant having higher thermostability than the parent cutinase.

24. A method of producing a cutinase variant, which method comprises:

a) selecting a parent fungal cutinase,

b) identifying one or more amino acid residues in the parent cutinase at positions which are:

i) within 17 Å from the location of the N-terminal amino acid (as calculated from amino acid residues in a crystal structure), and/or

ii) within 20 positions from the N-terminal amino acid, and

c) making alterations each of which is an insertion, a deletion or a substitution of the amino acid residue,

d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b),

e) preparing the variant resulting from steps b-d,

f) testing the thermostability of the variant,

g) optionally repeating steps b-f,

h) selecting a variant having higher thermostability than the parent cutinase, and

i) producing the variant to obtain the cutinase variant.

25. A process for enzymatic hydrolysis of a cyclic oligomer of poly(ethylene terephthalate), which process comprises treating the cyclic oligomer with a variant of a parent fungal cutinase, which variant comprises substitution of one or more amino acid residues at a position which is located:

i) within 17 Å from the location of the N-terminal amino acid (as calculated from amino acid residues in a crystal structure), and/or

ii) within 20 positions from the N-terminal amino acid.

26. The process of the preceding claim, in which the cyclic oligomer is cyclic tri(ethylene terephthalate).

27. The process of claim 25 or 26 wherein the treatment is done at 60-75°C, preferably at 65-70°C.

28. The process of any of claims 25-27 wherein the cyclic oligomer is present in and on the fibers of a polyester containing fabric or yarn.

29. The process of any of claims 25-28 which further comprises subsequently rinsing the fabric or yarn, preferably rinsing with an aqueous solution having a pH in the range of from about pH 7 to about pH 11.

30. A detergent composition comprising a surfactant and the variant of any of claims 1-18.

31. A method for detecting cutinase activity in a sample, comprising incubating the sample with terephthalic acid bis(2-hydroxyethyl)ester dibenzoate and detecting hydrolysis of said ester.

Fig. 1

3D structure of cutinase from *Humicola insolens*

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ATOM      1  N   GLY A   3      24.424  -7.935  18.390  1.00 46.73
ATOM      2  CA  GLY A   3      23.848  -8.994  17.546  1.00 42.29
ATOM      3  C   GLY A   3      24.396 -10.112  16.727  1.00 37.35
ATOM      4  O   GLY A   3      25.347 -10.913  16.728  1.00 35.38
ATOM      5  N   ALA A   4      23.664 -10.625  15.797  1.00 34.53
ATOM      6  CA  ALA A   4      23.051 -10.874  14.555  1.00 30.95
ATOM      7  C   ALA A   4      21.574 -11.246  14.920  1.00 28.33
ATOM      8  O   ALA A   4      20.677 -10.499  14.446  1.00 22.94
ATOM      9  CB  ALA A   4      23.574 -11.780  13.556  1.00 26.92
ATOM     10  N   ILE A   5      21.583 -12.058  16.043  1.00 26.48
ATOM     11  CA  ILE A   5      20.281 -12.289  16.637  1.00 25.65
ATOM     12  C   ILE A   5      20.316 -12.151  18.118  1.00 22.40
ATOM     13  O   ILE A   5      21.060 -12.888  18.717  1.00 24.74
ATOM     14  CB  ILE A   5      19.724 -13.683  16.524  1.00 26.04
ATOM     15  CG1 ILE A   5      19.852 -13.927  15.050  1.00 29.85
ATOM     16  CG2 ILE A   5      18.374 -13.558  17.159  1.00 20.48
ATOM     17  CD1 ILE A   5      19.066 -15.133  14.709  1.00 27.96
ATOM     18  N   GLU A   6      19.461 -11.377  18.668  1.00 20.52
ATOM     19  CA  GLU A   6      19.207 -11.015  20.040  1.00 17.94
ATOM     20  C   GLU A   6      17.711 -11.027  20.432  1.00 17.76
ATOM     21  O   GLU A   6      16.931 -10.165  19.990  1.00 17.60
ATOM     22  CB  GLU A   6      19.809  -9.614  20.199  1.00 14.22
ATOM     23  CG  GLU A   6      21.232  -9.374  20.385  1.00 16.71
ATOM     24  CD  GLU A   6      22.148 -10.387  21.030  1.00 34.47
ATOM     25  OE1 GLU A   6      21.634 -11.347  21.693  1.00 49.57
ATOM     26  OE2 GLU A   6      23.410 -10.310  20.975  1.00 37.43
ATOM     27  N   ASN A   7      17.375 -11.895  21.333  1.00 21.67
ATOM     28  CA  ASN A   7      16.070 -11.854  21.846  1.00 24.04
ATOM     29  C   ASN A   7      15.927 -11.488  23.238  1.00 22.08
ATOM     30  O   ASN A   7      15.098 -12.179  23.820  1.00 24.00
ATOM     31  CB  ASN A   7      15.468 -13.307  21.820  1.00 25.06
ATOM     32  CG  ASN A   7      15.039 -13.160  20.341  1.00 38.52
ATOM     33  OD1 ASN A   7      15.519 -14.147  19.759  1.00 48.45
ATOM     34  ND2 ASN A   7      14.318 -12.081  19.968  1.00 36.89
ATOM     35  N   GLY A   8      16.671 -10.813  23.926  1.00 23.56
ATOM     36  CA  GLY A   8      16.654 -10.628  25.363  1.00 23.69
ATOM     37  C   GLY A   8      15.366 -10.247  25.984  1.00 22.72
ATOM     38  O   GLY A   8      14.967 -10.939  26.867  1.00 32.25
ATOM     39  N   LEU A   9      14.785  -9.144  25.755  1.00 23.61
ATOM     40  CA  LEU A   9      13.470  -8.753  26.033  1.00 23.73
ATOM     41  C   LEU A   9      12.559  -9.961  25.782  1.00 25.93
ATOM     42  O   LEU A   9      11.494 -10.054  26.480  1.00 30.47
ATOM     43  CB  LEU A   9      12.971  -7.621  25.105  1.00  5.84
ATOM     44  CG  LEU A   9      11.556  -7.227  25.470  1.00 23.25
ATOM     45  CD1 LEU A   9      11.422  -6.765  26.968  1.00 20.21
ATOM     46  CD2 LEU A   9      11.009  -6.071  24.714  1.00 17.64
ATOM     47  N   GLU A  10      12.775 -10.786  24.773  1.00 29.56
ATOM     48  CA  GLU A  10      11.635 -11.681  24.484  1.00 33.93
ATOM     49  C   GLU A  10      11.640 -12.872  25.412  1.00 32.18
ATOM     50  O   GLU A  10      10.600 -13.159  25.996  1.00 36.67
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ATOM     51  CB  GLU A  10      11.513 -11.996  23.012  1.00 40.97
ATOM     52  CG  GLU A  10      10.054 -12.303  22.745  1.00 51.96
ATOM     53  CD  GLU A  10       9.570 -11.711  21.437  1.00 54.08
ATOM     54  OE1 GLU A  10      10.488 -11.440  20.635  1.00 48.22
ATOM     55  OE2 GLU A  10       8.323 -11.643  21.471  1.00 52.39
ATOM     56  N   SER A  11      12.822 -13.334  25.688  1.00 29.58
ATOM     57  CA  SER A  11      12.993 -14.455  26.645  1.00 35.25
ATOM     58  C   SER A  11      13.403 -14.012  28.047  1.00 39.86
ATOM     59  O   SER A  11      13.688 -14.790  28.919  1.00 43.72
ATOM     60  CB  SER A  11      14.053 -15.364  25.983  1.00 33.73
ATOM     61  OG  SER A  11      15.275 -14.620  25.928  1.00 46.98
ATOM     62  N   GLY A  12      13.467 -12.802  28.456  1.00 41.40
ATOM     63  CA  GLY A  12      13.841 -12.332  29.752  1.00 45.34
ATOM     64  C   GLY A  12      12.673 -12.562  30.694  1.00 47.62
ATOM     65  O   GLY A  12      11.485 -12.335  30.335  1.00 50.76
ATOM     66  N   SER A  13      12.969 -12.900  31.936  1.00 48.09
ATOM     67  CA  SER A  13      11.974 -13.158  32.995  1.00 45.26
ATOM     68  C   SER A  13      11.509 -11.933  33.772  1.00 39.53
ATOM     69  O   SER A  13      12.563 -11.204  33.992  1.00 36.30
ATOM     70  CB  SER A  13      12.708 -14.006  34.101  1.00 51.20
ATOM     71  OG  SER A  13      12.006 -13.947  35.338  1.00 57.14
ATOM     72  N   ALA A  14      10.256 -11.785  34.214  1.00 35.22
ATOM     73  CA  ALA A  14      10.068 -10.530  34.964  1.00 34.78
ATOM     74  C   ALA A  14      10.574 -10.620  36.417  1.00 37.51
ATOM     75  O   ALA A  14      10.809  -9.584  37.113  1.00 38.41
ATOM     76  CB  ALA A  14       8.714  -9.915  34.903  1.00 32.71
ATOM     77  N   ASN A  15      11.039 -11.834  36.737  1.00 38.85
ATOM     78  CA  ASN A  15      11.715 -12.086  37.963  1.00 43.49
ATOM     79  C   ASN A  15      13.073 -11.411  37.953  1.00 46.45
ATOM     80  O   ASN A  15      13.453 -11.022  39.022  1.00 52.50
ATOM     81  CB  ASN A  15      12.088 -13.533  38.207  1.00 53.08
ATOM     82  CG  ASN A  15      10.772 -14.226  38.553  1.00 71.86
ATOM     83  OD1 ASN A  15       9.837 -13.535  38.998  1.00 71.73
ATOM     84  ND2 ASN A  15      10.866 -15.523  38.267  1.00 77.71
ATOM     85  N   ALA A  16      13.712 -11.305  36.812  1.00 46.73
ATOM     86  CA  ALA A  16      14.915 -10.470  36.743  1.00 41.22
ATOM     87  C   ALA A  16      15.031  -9.286  35.798  1.00 36.70
ATOM     88  O   ALA A  16      16.027  -9.254  35.075  1.00 37.67
ATOM     89  CB  ALA A  16      15.903 -11.545  36.301  1.00 41.80
ATOM     90  N   CYS A  17      14.300  -8.227  35.843  1.00 30.62
ATOM     91  CA  CYS A  17      14.614  -7.093  34.997  1.00 31.78
ATOM     92  C   CYS A  17      16.024  -6.579  35.149  1.00 32.94
ATOM     93  O   CYS A  17      16.744  -6.850  36.113  1.00 39.10
ATOM     94  CB  CYS A  17      13.679  -5.881  35.138  1.00 28.00
ATOM     95  SG  CYS A  17      12.048  -6.583  34.858  1.00 24.72
ATOM     96  N   PRO A  18      16.529  -5.910  34.092  1.00 30.49
ATOM     97  CA  PRO A  18      17.994  -5.626  33.971  1.00 22.04
ATOM     98  C   PRO A  18      18.178  -4.138  34.241  1.00 20.15
ATOM     99  O   PRO A  18      17.085  -3.459  34.370  1.00 17.83
ATOM    100  CB  PRO A  18      18.353  -6.003  32.559  1.00 19.20
ATOM    101  CG  PRO A  18      17.044  -6.595  32.101  1.00 20.16
ATOM    102  CD  PRO A  18      15.903  -5.936  32.792  1.00 24.35
ATOM    103  N   ASP A  19      19.428  -3.652  34.011  1.00 14.85
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ATOM	104	CA	ASP	A	19	19.451	-2.168	34.226	1.00	16.59
ATOM	105	C	ASP	A	19	18.739	-1.367	33.156	1.00	20.42
ATOM	106	O	ASP	A	19	18.311	-0.242	33.430	1.00	23.84
ATOM	107	CB	ASP	A	19	20.896	-1.818	34.485	1.00	27.25
ATOM	108	CG	ASP	A	19	21.433	-2.389	35.793	1.00	42.30
ATOM	109	OD1	ASP	A	19	21.162	-3.549	36.297	1.00	53.52
ATOM	110	OD2	ASP	A	19	22.251	-1.719	36.543	1.00	54.02
ATOM	111	N	ALA	A	20	18.646	-1.780	31.895	1.00	20.18
ATOM	112	CA	ALA	A	20	18.066	-1.036	30.809	1.00	17.43
ATOM	113	C	ALA	A	20	17.713	-2.087	29.703	1.00	16.06
ATOM	114	O	ALA	A	20	18.334	-3.172	29.860	1.00	9.45
ATOM	115	CB	ALA	A	20	18.975	-0.048	30.100	1.00	12.07
ATOM	116	N	ILE	A	21	16.814	-1.602	28.829	1.00	8.47
ATOM	117	CA	ILE	A	21	16.657	-2.583	27.753	1.00	9.23
ATOM	118	C	ILE	A	21	16.952	-1.745	26.486	1.00	14.77
ATOM	119	O	ILE	A	21	16.681	-0.473	26.403	1.00	12.01
ATOM	120	CB	ILE	A	21	15.208	-2.984	27.837	1.00	16.28
ATOM	121	CG1	ILE	A	21	14.851	-3.898	28.956	1.00	15.55
ATOM	122	CG2	ILE	A	21	14.689	-3.671	26.514	1.00	13.71
ATOM	123	CD1	ILE	A	21	13.401	-3.879	29.372	1.00	6.12
ATOM	124	N	LEU	A	22	17.432	-2.451	25.391	1.00	12.24
ATOM	125	CA	LEU	A	22	17.665	-1.774	24.087	1.00	11.27
ATOM	126	C	LEU	A	22	16.849	-2.517	23.038	1.00	14.60
ATOM	127	O	LEU	A	22	16.908	-3.781	22.850	1.00	9.78
ATOM	128	CB	LEU	A	22	19.087	-1.865	23.693	1.00	10.96
ATOM	129	CG	LEU	A	22	19.493	-1.543	22.257	1.00	10.32
ATOM	130	CD1	LEU	A	22	19.311	-0.081	21.900	1.00	4.72
ATOM	131	CD2	LEU	A	22	20.990	-1.842	22.156	1.00	7.42
ATOM	132	N	ILE	A	23	16.038	-1.815	22.242	1.00	15.13
ATOM	133	CA	ILE	A	23	15.298	-2.459	21.115	1.00	18.06
ATOM	134	C	ILE	A	23	15.916	-1.771	19.901	1.00	17.42
ATOM	135	O	ILE	A	23	16.117	-0.519	19.795	1.00	19.31
ATOM	136	CB	ILE	A	23	13.820	-2.194	21.392	1.00	18.16
ATOM	137	CG1	ILE	A	23	13.208	-3.076	22.447	1.00	14.23
ATOM	138	CG2	ILE	A	23	12.787	-2.167	20.247	1.00	13.19
ATOM	139	CD1	ILE	A	23	12.142	-2.065	22.976	1.00	20.41
ATOM	140	N	PHE	A	24	16.218	-2.548	18.940	1.00	14.59
ATOM	141	CA	PHE	A	24	16.859	-2.159	17.671	1.00	11.72
ATOM	142	C	PHE	A	24	16.347	-2.719	16.353	1.00	7.25
ATOM	143	O	PHE	A	24	16.095	-3.998	16.161	1.00	3.47
ATOM	144	CB	PHE	A	24	18.195	-2.855	17.658	1.00	12.61
ATOM	145	CG	PHE	A	24	19.015	-2.150	16.716	1.00	10.72
ATOM	146	CD1	PHE	A	24	19.457	-0.844	16.913	1.00	13.08
ATOM	147	CD2	PHE	A	24	19.325	-2.852	15.558	1.00	6.61
ATOM	148	CE1	PHE	A	24	20.232	-0.187	15.983	1.00	4.86
ATOM	149	CE2	PHE	A	24	20.061	-2.218	14.545	1.00	7.61
ATOM	150	CZ	PHE	A	24	20.550	-0.823	14.804	1.00	8.78
ATOM	151	N	ALA	A	25	16.037	-1.700	15.449	1.00	6.32
ATOM	152	CA	ALA	A	25	15.662	-2.158	14.068	1.00	7.18
ATOM	153	C	ALA	A	25	16.851	-1.976	13.055	1.00	8.59
ATOM	154	O	ALA	A	25	17.518	-1.000	13.133	1.00	5.95
ATOM	155	CB	ALA	A	25	14.488	-1.402	13.562	1.00	8.27
ATOM	156	N	ARG	A	26	17.174	-3.032	12.325	1.00	8.84

	ATOM	157	CA	ARG	A	26	18.134	-3.278	11.277	1.00	4.04
	ATOM	158	C	ARG	A	26	17.691	-2.694	9.894	1.00	7.67
	ATOM	159	O	ARG	A	26	16.527	-2.361	9.525	1.00	9.36
	ATOM	160	CB	ARG	A	26	18.581	-4.659	10.756	1.00	6.06
	ATOM	161	CG	ARG	A	26	17.705	-5.741	10.439	1.00	5.08
	ATOM	162	CD	ARG	A	26	18.069	-7.224	10.382	1.00	6.73
	ATOM	163	NE	ARG	A	26	17.000	-8.053	9.708	1.00	9.04
	ATOM	164	CZ	ARG	A	26	15.724	-8.206	9.912	1.00	7.06
	ATOM	165	NH1	ARG	A	26	15.085	-7.535	10.895	1.00	22.93
	ATOM	166	NH2	ARG	A	26	14.809	-8.825	9.346	1.00	7.89
	ATOM	167	N	GLY	A	27	18.761	-2.539	9.092	1.00	7.71
	ATOM	168	CA	GLY	A	27	18.537	-1.888	7.782	1.00	5.34
	ATOM	169	C	GLY	A	27	18.063	-2.896	6.862	1.00	4.70
	ATOM	170	O	GLY	A	27	18.155	-4.139	7.075	1.00	13.14
	ATOM	171	N	SER	A	28	17.562	-2.612	5.765	1.00	11.82
	ATOM	172	CA	SER	A	28	17.108	-3.325	4.615	1.00	14.72
	ATOM	173	C	SER	A	28	18.214	-4.327	4.142	1.00	7.74
	ATOM	174	O	SER	A	28	19.286	-3.973	4.083	1.00	6.71
	ATOM	175	CB	SER	A	28	16.460	-2.352	3.538	1.00	6.38
	ATOM	176	OG	SER	A	28	16.819	-0.978	3.833	1.00	28.10
	ATOM	177	N	THR	A	29	17.942	-5.634	4.241	1.00	4.79
	ATOM	178	CA	THR	A	29	18.562	-6.763	3.914	1.00	8.71
	ATOM	179	C	THR	A	29	19.500	-7.271	4.985	1.00	14.00
	ATOM	180	O	THR	A	29	20.162	-8.326	4.713	1.00	17.68
	ATOM	181	CB	THR	A	29	19.454	-6.680	2.617	1.00	14.90
	ATOM	182	OG1	THR	A	29	20.736	-6.066	2.595	1.00	14.00
	ATOM	183	CG2	THR	A	29	18.785	-5.888	1.561	1.00	15.59
	ATOM	184	N	GLU	A	30	19.740	-6.599	6.105	1.00	14.52
	ATOM	185	CA	GLU	A	30	20.677	-7.266	7.056	1.00	14.10
	ATOM	186	C	GLU	A	30	20.092	-8.513	7.647	1.00	13.07
	ATOM	187	O	GLU	A	30	18.916	-8.726	7.705	1.00	19.98
	ATOM	188	CB	GLU	A	30	21.228	-6.371	8.072	1.00	15.45
	ATOM	189	CG	GLU	A	30	21.166	-4.945	7.709	1.00	8.37
	ATOM	190	CD	GLU	A	30	22.073	-4.143	8.637	1.00	23.08
	ATOM	191	OE1	GLU	A	30	21.395	-3.328	9.284	1.00	19.26
	ATOM	192	OE2	GLU	A	30	23.317	-4.327	8.712	1.00	19.71
	ATOM	193	N	PRO	A	31	20.875	-9.479	7.918	1.00	13.09
	ATOM	194	CA	PRO	A	31	20.477	-10.818	8.402	1.00	14.56
	ATOM	195	C	PRO	A	31	20.167	-10.698	9.895	1.00	18.27
	ATOM	196	O	PRO	A	31	20.148	-9.636	10.392	1.00	20.45
	ATOM	197	CB	PRO	A	31	21.690	-11.692	8.215	1.00	10.95
	ATOM	198	CG	PRO	A	31	22.790	-10.664	8.455	1.00	11.24
	ATOM	199	CD	PRO	A	31	22.350	-9.316	7.864	1.00	13.71
	ATOM	200	N	GLY	A	32	19.612	-11.689	10.472	1.00	18.99
	ATOM	201	CA	GLY	A	32	19.205	-11.774	11.816	1.00	13.53
	ATOM	202	C	GLY	A	32	18.133	-10.808	12.188	1.00	16.62
	ATOM	203	O	GLY	A	32	17.345	-10.294	11.411	1.00	17.01
	ATOM	204	N	ASN	A	33	18.055	-10.528	13.468	1.00	16.15
	ATOM	205	CA	ASN	A	33	17.290	-9.346	13.823	1.00	14.74
	ATOM	206	C	ASN	A	33	18.294	-8.273	14.230	1.00	15.46
	ATOM	207	O	ASN	A	33	17.774	-7.184	14.575	1.00	15.90
	ATOM	208	CB	ASN	A	33	16.241	-9.663	14.867	1.00	17.42
	ATOM	209	CG	ASN	A	33	16.827	-10.201	16.127	1.00	17.97

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ATOM    210  OD1 ASN A  33      16.112 -10.395  17.089  1.00 19.05
ATOM    211  ND2 ASN A  33      18.074 -10.460  16.112  1.00 13.29
ATOM    212  N   MET A  34      19.633  -8.378  14.282  1.00 14.22
ATOM    213  CA  MET A  34      20.282  -7.171  14.751  1.00 12.97
ATOM    214  C   MET A  34      21.142  -6.663  13.611  1.00 19.02
ATOM    215  O   MET A  34      21.654  -5.512  13.713  1.00 26.04
ATOM    216  CB  MET A  34      21.202  -7.329  15.859  1.00 13.39
ATOM    217  CG  MET A  34      20.579  -7.713  17.163  1.00  9.02
ATOM    218  SD  MET A  34      20.175  -6.316  18.069  1.00  9.13
ATOM    219  CE  MET A  34      21.481  -5.121  18.095  1.00  4.11
ATOM    220  N   GLY A  35      21.259  -7.446  12.550  1.00 19.99
ATOM    221  CA  GLY A  35      22.071  -7.135  11.418  1.00 14.30
ATOM    222  C   GLY A  35      23.511  -7.340  11.764  1.00 17.58
ATOM    223  O   GLY A  35      23.965  -7.724  12.842  1.00 12.78
ATOM    224  N   ILE A  36      24.450  -6.839  10.950  1.00 20.63
ATOM    225  CA  ILE A  36      25.833  -7.029  11.277  1.00 17.71
ATOM    226  C   ILE A  36      26.609  -5.714  11.280  1.00 16.15
ATOM    227  O   ILE A  36      27.865  -5.618  11.662  1.00 20.30
ATOM    228  CB  ILE A  36      26.412  -8.070  10.327  1.00 30.19
ATOM    229  CG1 ILE A  36      26.088  -7.448   8.959  1.00 31.16
ATOM    230  CG2 ILE A  36      25.944  -9.490  10.543  1.00 15.68
ATOM    231  CD1 ILE A  36      26.922  -8.149   7.958  1.00 34.10
ATOM    232  N   THR A  37      25.905  -4.589  11.040  1.00 13.00
ATOM    233  CA  THR A  37      26.825  -3.396  11.141  1.00  9.67
ATOM    234  C   THR A  37      26.587  -2.513  12.350  1.00 15.44
ATOM    235  O   THR A  37      27.040  -3.055  13.410  1.00 20.20
ATOM    236  CB  THR A  37      26.592  -2.679   9.818  1.00 14.13
ATOM    237  OG1 THR A  37      25.241  -2.212   9.503  1.00 22.62
ATOM    238  CG2 THR A  37      26.949  -3.739   8.800  1.00  2.29
ATOM    239  N   VAL A  38      25.733  -1.493  12.249  1.00 11.92
ATOM    240  CA  VAL A  38      25.237  -0.800  13.411  1.00 15.22
ATOM    241  C   VAL A  38      24.588  -1.455  14.612  1.00 14.68
ATOM    242  O   VAL A  38      24.906  -1.185  15.733  1.00 15.89
ATOM    243  CB  VAL A  38      24.124   0.180  12.855  1.00 14.13
ATOM    244  CG1 VAL A  38      23.663   0.897  14.167  1.00 13.55
ATOM    245  CG2 VAL A  38      24.570   1.025  11.670  1.00  6.75
ATOM    246  N   GLY A  39      23.745  -2.410  14.677  1.00 14.24
ATOM    247  CA  GLY A  39      23.135  -3.151  15.746  1.00 11.03
ATOM    248  C   GLY A  39      24.096  -3.586  16.791  1.00 13.34
ATOM    249  O   GLY A  39      24.131  -3.181  17.934  1.00 15.13
ATOM    250  N   PRO A  40      25.067  -4.340  16.352  1.00 14.70
ATOM    251  CA  PRO A  40      26.094  -5.025  17.171  1.00 13.44
ATOM    252  C   PRO A  40      27.010  -3.909  17.589  1.00 11.81
ATOM    253  O   PRO A  40      27.346  -3.871  18.764  1.00 12.79
ATOM    254  CB  PRO A  40      26.723  -6.111  16.279  1.00  8.43
ATOM    255  CG  PRO A  40      25.873  -6.243  14.950  1.00  4.84
ATOM    256  CD  PRO A  40      25.198  -4.902  14.995  1.00 12.36
ATOM    257  N   ALA A  41      27.226  -2.979  16.695  1.00  7.41
ATOM    258  CA  ALA A  41      28.066  -1.962  17.278  1.00 11.03
ATOM    259  C   ALA A  41      27.378  -1.206  18.439  1.00 14.87
ATOM    260  O   ALA A  41      28.028  -0.503  19.274  1.00 14.26
ATOM    261  CB  ALA A  41      28.579  -0.905  16.313  1.00  7.17
ATOM    262  N   LEU A  42      26.135  -0.811  18.237  1.00 11.87
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ATOM	263	CA	LEU	A	42	25.487	-0.048	19.300	1.00	12.36
ATOM	264	C	LEU	A	42	25.337	-0.856	20.624	1.00	11.94
ATOM	265	O	LEU	A	42	25.423	-0.397	21.730	1.00	8.33
ATOM	266	CB	LEU	A	42	24.036	0.168	18.811	1.00	13.24
ATOM	267	CG	LEU	A	42	23.272	1.160	19.676	1.00	6.90
ATOM	268	CD1	LEU	A	42	24.108	2.419	19.962	1.00	6.62
ATOM	269	CD2	LEU	A	42	21.991	1.580	18.943	1.00	7.11
ATOM	270	N	ALA	A	43	24.905	-2.095	20.482	1.00	10.88
ATOM	271	CA	ALA	A	43	24.761	-3.027	21.553	1.00	12.37
ATOM	272	C	ALA	A	43	26.106	-3.136	22.252	1.00	15.45
ATOM	273	O	ALA	A	43	25.958	-2.743	23.433	1.00	20.80
ATOM	274	CB	ALA	A	43	24.148	-4.324	21.002	1.00	9.60
ATOM	275	N	ASN	A	44	27.263	-3.440	21.636	1.00	16.91
ATOM	276	CA	ASN	A	44	28.454	-3.434	22.439	1.00	20.33
ATOM	277	C	ASN	A	44	28.717	-2.044	23.113	1.00	17.66
ATOM	278	O	ASN	A	44	29.019	-1.991	24.301	1.00	17.06
ATOM	279	CB	ASN	A	44	29.756	-3.695	21.625	1.00	35.48
ATOM	280	CG	ASN	A	44	29.564	-5.115	21.138	1.00	58.23
ATOM	281	OD1	ASN	A	44	30.013	-5.403	20.034	1.00	79.77
ATOM	282	ND2	ASN	A	44	28.908	-5.945	21.921	1.00	70.10
ATOM	283	N	GLY	A	45	28.682	-0.988	22.297	1.00	14.39
ATOM	284	CA	GLY	A	45	29.015	0.221	22.976	1.00	11.65
ATOM	285	C	GLY	A	45	28.175	0.255	24.234	1.00	14.30
ATOM	286	O	GLY	A	45	28.529	0.582	25.385	1.00	10.77
ATOM	287	N	LEU	A	46	26.861	0.099	24.065	1.00	16.88
ATOM	288	CA	LEU	A	46	25.968	0.248	25.207	1.00	16.29
ATOM	289	C	LEU	A	46	26.395	-0.651	26.346	1.00	13.48
ATOM	290	O	LEU	A	46	26.579	-0.325	27.462	1.00	7.75
ATOM	291	CB	LEU	A	46	24.608	-0.243	24.847	1.00	19.46
ATOM	292	CG	LEU	A	46	23.642	0.551	25.664	1.00	13.97
ATOM	293	CD1	LEU	A	46	24.089	1.994	25.563	1.00	13.99
ATOM	294	CD2	LEU	A	46	22.275	0.465	25.038	1.00	32.18
ATOM	295	N	GLU	A	47	26.523	-1.890	25.882	1.00	15.90
ATOM	296	CA	GLU	A	47	26.910	-2.886	26.909	1.00	24.03
ATOM	297	C	GLU	A	47	28.140	-2.500	27.702	1.00	24.14
ATOM	298	O	GLU	A	47	28.722	-3.203	28.500	1.00	27.24
ATOM	299	CB	GLU	A	47	27.147	-4.206	26.204	1.00	33.33
ATOM	300	CG	GLU	A	47	27.386	-5.254	27.245	1.00	51.29
ATOM	301	CD	GLU	A	47	27.661	-6.560	26.524	1.00	68.40
ATOM	302	OE1	GLU	A	47	26.741	-7.007	25.777	1.00	66.37
ATOM	303	OE2	GLU	A	47	28.856	-6.921	26.830	1.00	78.70
ATOM	304	N	SER	A	48	28.992	-1.626	27.215	1.00	27.50
ATOM	305	CA	SER	A	48	30.331	-1.518	27.789	1.00	25.23
ATOM	306	C	SER	A	48	30.108	-0.555	28.926	1.00	26.91
ATOM	307	O	SER	A	48	31.124	-0.058	29.462	1.00	33.39
ATOM	308	CB	SER	A	48	31.116	-0.990	26.621	1.00	21.90
ATOM	309	OG	SER	A	48	31.294	0.422	26.483	1.00	27.87
ATOM	310	N	HIS	A	49	28.826	-0.101	28.995	1.00	25.04
ATOM	311	CA	HIS	A	49	28.542	0.955	29.956	1.00	19.72
ATOM	312	C	HIS	A	49	27.480	0.461	30.950	1.00	22.55
ATOM	313	O	HIS	A	49	27.186	1.089	31.898	1.00	27.93
ATOM	314	CB	HIS	A	49	28.094	2.197	29.463	1.00	16.13
ATOM	315	CG	HIS	A	49	28.806	3.036	28.520	1.00	39.79

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ATOM    316  ND1 HIS A  49      29.564   4.058  28.953  1.00 45.66
ATOM    317  CD2 HIS A  49      28.776   3.070  27.197  1.00 46.91
ATOM    318  CE1 HIS A  49      30.028   4.750  27.979  1.00 45.87
ATOM    319  NE2 HIS A  49      29.544   4.139  26.934  1.00 50.84
ATOM    320  N   ILE A  50      27.009  -0.703  30.715  1.00 18.34
ATOM    321  CA  ILE A  50      25.874  -1.129  31.415  1.00 19.89
ATOM    322  C   ILE A  50      25.917  -2.629  31.146  1.00 26.29
ATOM    323  O   ILE A  50      25.322  -3.023  30.168  1.00 25.33
ATOM    324  CB  ILE A  50      24.527  -0.535  31.008  1.00 10.50
ATOM    325  CG1 ILE A  50      24.340   0.906  31.292  1.00  4.97
ATOM    326  CG2 ILE A  50      23.466  -1.298  31.697  1.00 12.96
ATOM    327  CD1 ILE A  50      23.413   1.845  30.602  1.00 16.65
ATOM    328  N   ARG A  51      26.707  -3.256  32.066  1.00 31.77
ATOM    329  CA  ARG A  51      26.887  -4.714  32.107  1.00 29.06
ATOM    330  C   ARG A  51      25.457  -5.331  32.170  1.00 32.68
ATOM    331  O   ARG A  51      25.396  -6.363  31.512  1.00 37.16
ATOM    332  N   ASN A  52      24.380  -4.817  32.788  1.00 28.48
ATOM    333  CA  ASN A  52      23.284  -5.767  32.832  1.00 26.39
ATOM    334  C   ASN A  52      22.176  -5.178  31.993  1.00 27.75
ATOM    335  O   ASN A  52      21.333  -4.488  32.636  1.00 26.68
ATOM    336  CB  ASN A  52      22.750  -5.884  34.232  1.00 34.86
ATOM    337  CG  ASN A  52      21.637  -6.879  34.271  1.00 39.54
ATOM    338  OD1 ASN A  52      20.781  -6.541  35.095  1.00 54.31
ATOM    339  ND2 ASN A  52      21.611  -7.954  33.503  1.00 48.82
ATOM    340  N   ILE A  53      22.127  -5.699  30.800  1.00 24.42
ATOM    341  CA  ILE A  53      21.261  -5.092  29.772  1.00 20.15
ATOM    342  C   ILE A  53      20.585  -6.151  28.912  1.00 17.63
ATOM    343  O   ILE A  53      21.020  -7.349  28.917  1.00 18.01
ATOM    344  CB  ILE A  53      22.245  -4.297  28.880  1.00 14.09
ATOM    345  CG1 ILE A  53      21.682  -3.257  27.936  1.00 22.91
ATOM    346  CG2 ILE A  53      22.907  -5.321  27.946  1.00 16.37
ATOM    347  CD1 ILE A  53      22.877  -2.315  27.622  1.00 38.17
ATOM    348  N   TRP A  54      19.447  -5.880  28.383  1.00 15.19
ATOM    349  CA  TRP A  54      18.804  -6.889  27.567  1.00 17.96
ATOM    350  C   TRP A  54      18.803  -6.230  26.151  1.00 19.82
ATOM    351  O   TRP A  54      18.340  -5.059  25.985  1.00 18.37
ATOM    352  CB  TRP A  54      17.364  -7.046  27.998  1.00 23.18
ATOM    353  CG  TRP A  54      16.949  -7.932  29.100  1.00 24.57
ATOM    354  CD1 TRP A  54      17.757  -8.727  29.895  1.00 24.46
ATOM    355  CD2 TRP A  54      15.595  -8.164  29.603  1.00 30.21
ATOM    356  NE1 TRP A  54      17.004  -9.372  30.858  1.00 25.87
ATOM    357  CE2 TRP A  54      15.692  -9.039  30.700  1.00 24.92
ATOM    358  CE3 TRP A  54      14.358  -7.633  29.243  1.00 36.26
ATOM    359  CZ2 TRP A  54      14.611  -9.442  31.432  1.00 19.75
ATOM    360  CZ3 TRP A  54      13.316  -8.042  30.009  1.00 32.94
ATOM    361  CH2 TRP A  54      13.451  -8.916  31.068  1.00 23.02
ATOM    362  N   ILE A  55      19.063  -7.152  25.204  1.00 15.21
ATOM    363  CA  ILE A  55      19.178  -6.655  23.838  1.00 12.41
ATOM    364  C   ILE A  55      18.091  -7.215  22.962  1.00 11.40
ATOM    365  O   ILE A  55      17.955  -8.378  22.680  1.00  7.34
ATOM    366  CB  ILE A  55      20.546  -6.962  23.201  1.00 16.44
ATOM    367  CG1 ILE A  55      21.939  -6.409  23.702  1.00  8.75
ATOM    368  CG2 ILE A  55      20.384  -6.460  21.750  1.00 21.77
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ATOM	369	CD1	ILE	A	55	21.767	-5.582	24.863	1.00	16.23
ATOM	370	N	GLN	A	56	17.226	-6.412	22.390	1.00	9.67
ATOM	371	CA	GLN	A	56	16.161	-7.016	21.619	1.00	10.90
ATOM	372	C	GLN	A	56	16.432	-6.621	20.143	1.00	13.08
ATOM	373	O	GLN	A	56	16.402	-5.393	19.953	1.00	10.32
ATOM	374	CB	GLN	A	56	14.786	-6.542	22.014	1.00	11.49
ATOM	375	CG	GLN	A	56	13.653	-7.256	21.316	1.00	23.47
ATOM	376	CD	GLN	A	56	13.789	-8.741	21.351	1.00	24.88
ATOM	377	OE1	GLN	A	56	13.610	-9.379	20.324	1.00	9.56
ATOM	378	NE2	GLN	A	56	14.119	-9.221	22.544	1.00	17.94
ATOM	379	N	GLY	A	57	16.288	-7.645	19.216	1.00	6.84
ATOM	380	CA	GLY	A	57	16.174	-7.019	17.841	1.00	16.15
ATOM	381	C	GLY	A	57	14.740	-7.085	17.267	1.00	13.72
ATOM	382	O	GLY	A	57	14.124	-8.016	17.752	1.00	12.70
ATOM	383	N	VAL	A	58	14.068	-6.264	16.525	1.00	12.73
ATOM	384	CA	VAL	A	58	12.739	-6.308	16.070	1.00	11.16
ATOM	385	C	VAL	A	58	12.715	-7.246	14.893	1.00	14.85
ATOM	386	O	VAL	A	58	13.234	-6.891	13.849	1.00	18.64
ATOM	387	CB	VAL	A	58	12.262	-4.984	15.352	1.00	6.54
ATOM	388	CG1	VAL	A	58	10.894	-4.974	14.731	1.00	5.89
ATOM	389	CG2	VAL	A	58	12.650	-3.840	16.331	1.00	5.86
ATOM	390	N	GLY	A	59	12.209	-8.465	15.008	1.00	21.96
ATOM	391	CA	GLY	A	59	12.120	-9.385	13.874	1.00	17.81
ATOM	392	C	GLY	A	59	10.645	-9.561	13.550	1.00	23.35
ATOM	393	O	GLY	A	59	9.919	-8.579	13.249	1.00	27.99
ATOM	394	N	GLY	A	60	10.166	-10.805	13.623	1.00	18.75
ATOM	395	CA	GLY	A	60	8.841	-11.142	13.285	1.00	11.46
ATOM	396	C	GLY	A	60	8.550	-10.833	11.851	1.00	14.56
ATOM	397	O	GLY	A	60	9.160	-11.439	11.003	1.00	16.32
ATOM	398	N	PRO	A	61	7.505	-10.103	11.612	1.00	12.10
ATOM	399	CA	PRO	A	61	7.123	-9.774	10.250	1.00	14.70
ATOM	400	C	PRO	A	61	8.230	-8.941	9.570	1.00	22.17
ATOM	401	O	PRO	A	61	8.143	-8.758	8.344	1.00	25.74
ATOM	402	CB	PRO	A	61	5.911	-8.860	10.332	1.00	14.30
ATOM	403	CG	PRO	A	61	5.880	-8.514	11.784	1.00	13.62
ATOM	404	CD	PRO	A	61	6.723	-9.417	12.576	1.00	12.29
ATOM	405	N	TYR	A	62	9.162	-8.257	10.292	1.00	21.56
ATOM	406	CA	TYR	A	62	9.973	-7.242	9.674	1.00	17.07
ATOM	407	C	TYR	A	62	11.133	-7.907	9.047	1.00	18.73
ATOM	408	O	TYR	A	62	12.132	-8.213	9.691	1.00	22.39
ATOM	409	CB	TYR	A	62	10.504	-6.401	10.803	1.00	17.51
ATOM	410	CG	TYR	A	62	11.461	-5.421	10.236	1.00	15.23
ATOM	411	CD1	TYR	A	62	11.343	-4.920	9.032	1.00	17.79
ATOM	412	CD2	TYR	A	62	12.465	-4.971	10.969	1.00	19.09
ATOM	413	CE1	TYR	A	62	12.206	-3.997	8.506	1.00	19.28
ATOM	414	CE2	TYR	A	62	13.438	-4.101	10.490	1.00	25.40
ATOM	415	CZ	TYR	A	62	13.327	-3.571	9.186	1.00	20.95
ATOM	416	OH	TYR	A	62	14.320	-2.649	8.791	1.00	14.70
ATOM	417	N	ASP	A	63	10.998	-8.419	7.816	1.00	19.47
ATOM	418	CA	ASP	A	63	12.137	-9.011	7.081	1.00	17.52
ATOM	419	C	ASP	A	63	13.027	-7.973	6.453	1.00	17.97
ATOM	420	O	ASP	A	63	13.628	-8.442	5.512	1.00	14.94
ATOM	421	CB	ASP	A	63	11.474	-9.873	6.015	1.00	17.16

ATOM	422	CG	ASP	A	63	10.563	-9.136	5.096	1.00	27.75
ATOM	423	OD1	ASP	A	63	10.049	-8.030	5.281	1.00	34.11
ATOM	424	OD2	ASP	A	63	10.300	-9.635	4.002	1.00	44.13
ATOM	425	N	ALA	A	64	13.089	-6.685	6.584	1.00	15.36
ATOM	426	CA	ALA	A	64	14.054	-5.725	6.098	1.00	17.14
ATOM	427	C	ALA	A	64	14.118	-5.780	4.589	1.00	21.10
ATOM	428	O	ALA	A	64	15.193	-5.861	3.968	1.00	23.12
ATOM	429	CB	ALA	A	64	15.458	-5.861	6.646	1.00	20.45
ATOM	430	N	ALA	A	65	12.946	-6.009	4.006	1.00	22.21
ATOM	431	CA	ALA	A	65	12.817	-6.072	2.565	1.00	21.81
ATOM	432	C	ALA	A	65	13.143	-4.857	1.745	1.00	21.76
ATOM	433	O	ALA	A	65	12.855	-3.801	2.229	1.00	23.60
ATOM	434	CB	ALA	A	65	11.384	-6.390	2.364	1.00	17.31
ATOM	435	N	LEU	A	66	13.401	-4.866	0.402	1.00	21.48
ATOM	436	CA	LEU	A	66	13.763	-3.581	-0.216	1.00	13.20
ATOM	437	C	LEU	A	66	12.469	-2.913	-0.452	1.00	13.90
ATOM	438	O	LEU	A	66	12.548	-1.767	-0.197	1.00	11.85
ATOM	439	CB	LEU	A	66	14.593	-3.602	-1.470	1.00	3.92
ATOM	440	CG	LEU	A	66	15.891	-4.308	-1.191	1.00	9.05
ATOM	441	CD1	LEU	A	66	16.509	-4.725	-2.438	1.00	12.78
ATOM	442	CD2	LEU	A	66	16.569	-3.119	-0.580	1.00	13.44
ATOM	443	N	ALA	A	67	11.413	-3.625	-0.801	1.00	14.94
ATOM	444	CA	ALA	A	67	10.253	-2.759	-1.277	1.00	12.42
ATOM	445	C	ALA	A	67	9.626	-1.879	-0.224	1.00	14.21
ATOM	446	O	ALA	A	67	9.218	-0.818	-0.643	1.00	14.29
ATOM	447	CB	ALA	A	67	9.089	-3.588	-1.781	1.00	3.90
ATOM	448	N	THR	A	68	9.494	-2.409	1.006	1.00	12.11
ATOM	449	CA	THR	A	68	8.780	-1.647	1.997	1.00	11.77
ATOM	450	C	THR	A	68	9.242	-0.214	2.219	1.00	13.05
ATOM	451	O	THR	A	68	8.597	0.683	2.766	1.00	11.13
ATOM	452	CB	THR	A	68	8.892	-2.488	3.241	1.00	13.93
ATOM	453	OG1	THR	A	68	10.145	-3.150	3.224	1.00	27.44
ATOM	454	CG2	THR	A	68	7.783	-3.459	3.087	1.00	13.39
ATOM	455	N	ASN	A	69	10.450	-0.057	1.808	1.00	7.59
ATOM	456	CA	ASN	A	69	11.020	1.236	1.791	1.00	8.76
ATOM	457	C	ASN	A	69	10.095	2.165	1.047	1.00	10.28
ATOM	458	O	ASN	A	69	9.950	3.345	1.305	1.00	5.30
ATOM	459	CB	ASN	A	69	12.461	1.251	1.231	1.00	5.54
ATOM	460	CG	ASN	A	69	13.374	1.207	2.398	1.00	15.08
ATOM	461	OD1	ASN	A	69	13.307	2.124	3.275	1.00	31.90
ATOM	462	ND2	ASN	A	69	14.048	0.099	2.360	1.00	4.51
ATOM	463	N	PHE	A	70	9.390	1.656	0.079	1.00	19.09
ATOM	464	CA	PHE	A	70	8.552	2.619	-0.631	1.00	21.80
ATOM	465	C	PHE	A	70	7.157	2.836	-0.123	1.00	23.36
ATOM	466	O	PHE	A	70	6.509	3.717	-0.724	1.00	25.74
ATOM	467	CB	PHE	A	70	8.547	2.386	-2.082	1.00	17.38
ATOM	468	CG	PHE	A	70	9.870	2.360	-2.770	1.00	15.72
ATOM	469	CD1	PHE	A	70	10.080	3.430	-3.576	1.00	5.15
ATOM	470	CD2	PHE	A	70	10.702	1.245	-2.497	1.00	7.61
ATOM	471	CE1	PHE	A	70	11.268	3.330	-4.191	1.00	16.05
ATOM	472	CE2	PHE	A	70	11.913	1.267	-3.168	1.00	22.23
ATOM	473	CZ	PHE	A	70	12.199	2.314	-4.016	1.00	9.57
ATOM	474	N	LEU	A	71	6.765	2.246	1.034	1.00	25.53

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ATOM    475  CA  LEU A  71       5.506   2.725   1.599  1.00 24.24
ATOM    476  C   LEU A  71       5.649   4.037   2.343  1.00 27.91
ATOM    477  O   LEU A  71       6.694   4.521   2.750  1.00 28.86
ATOM    478  CB  LEU A  71       5.150   1.635   2.535  1.00 19.99
ATOM    479  CG  LEU A  71       5.003   0.342   1.873  1.00 16.09
ATOM    480  CD1 LEU A  71       4.879  -0.764   2.885  1.00 18.12
ATOM    481  CD2 LEU A  71       3.786   0.546   1.000  1.00 18.24
ATOM    482  N   PRO A  72       4.535   4.663   2.529  1.00 33.01
ATOM    483  CA  PRO A  72       4.389   5.888   3.311  1.00 34.96
ATOM    484  C   PRO A  72       4.865   5.590   4.778  1.00 32.90
ATOM    485  O   PRO A  72       4.619   4.512   5.331  1.00 28.55
ATOM    486  CB  PRO A  72       2.983   6.453   3.095  1.00 32.98
ATOM    487  CG  PRO A  72       2.224   5.189   2.827  1.00 30.36
ATOM    488  CD  PRO A  72       3.188   4.093   2.380  1.00 33.56
ATOM    489  N   ARG A  73       5.601   6.610   5.221  1.00 27.54
ATOM    490  CA  ARG A  73       6.325   6.547   6.408  1.00 25.42
ATOM    491  C   ARG A  73       7.613   5.755   6.321  1.00 21.78
ATOM    492  O   ARG A  73       8.360   5.950   7.304  1.00 29.61
ATOM    493  CB  ARG A  73       5.469   5.978   7.549  1.00 24.29
ATOM    494  CG  ARG A  73       4.575   6.998   8.155  1.00 23.47
ATOM    495  CD  ARG A  73       3.818   6.793   9.360  1.00 29.73
ATOM    496  NE  ARG A  73       3.222   5.460   9.392  1.00 36.30
ATOM    497  CZ  ARG A  73       2.891   5.312  10.713  1.00 42.26
ATOM    498  NH1 ARG A  73       3.145   6.288  11.555  1.00 26.57
ATOM    499  NH2 ARG A  73       2.320   4.144  10.883  1.00 39.03
ATOM    500  N   GLY A  74       7.868   4.909   5.326  1.00  8.42
ATOM    501  CA  GLY A  74       9.120   4.291   5.332  1.00  5.06
ATOM    502  C   GLY A  74       9.243   2.858   5.508  1.00 12.74
ATOM    503  O   GLY A  74      10.256   2.286   5.317  1.00 16.46
ATOM    504  N   THR A  75       8.145   2.321   5.906  1.00 12.82
ATOM    505  CA  THR A  75       8.036   0.869   6.008  1.00 11.14
ATOM    506  C   THR A  75       6.625   0.428   6.134  1.00 10.64
ATOM    507  O   THR A  75       5.757   1.231   5.949  1.00  9.36
ATOM    508  CB  THR A  75       8.843   0.398   7.219  1.00  6.97
ATOM    509  OG1 THR A  75       8.938  -0.950   7.125  1.00  5.64
ATOM    510  CG2 THR A  75       8.108   0.865   8.603  1.00  6.30
ATOM    511  N   SER A  76       6.409  -0.858   6.259  1.00 10.07
ATOM    512  CA  SER A  76       5.061  -1.384   6.354  1.00 13.33
ATOM    513  C   SER A  76       4.405  -1.163   7.747  1.00 21.87
ATOM    514  O   SER A  76       5.228  -1.102   8.679  1.00 24.22
ATOM    515  CB  SER A  76       5.030  -2.832   6.083  1.00  4.81
ATOM    516  OG  SER A  76       5.327  -3.664   7.107  1.00 16.98
ATOM    517  N   GLN A  77       3.082  -1.100   7.911  1.00 24.90
ATOM    518  CA  GLN A  77       2.454  -1.020   9.166  1.00 23.85
ATOM    519  C   GLN A  77       2.643  -2.236  10.015  1.00 19.58
ATOM    520  O   GLN A  77       2.908  -2.140  11.203  1.00 15.15
ATOM    521  CB  GLN A  77       0.983  -0.703   9.217  1.00 32.64
ATOM    522  CG  GLN A  77       0.567  -0.580  10.642  1.00 49.56
ATOM    523  CD  GLN A  77       0.689   0.785  11.194  1.00 65.91
ATOM    524  OE1 GLN A  77       0.956   0.869  12.356  1.00 66.06
ATOM    525  NE2 GLN A  77       0.481   1.750  10.350  1.00 68.91
ATOM    526  N   ALA A  78       2.754  -3.376   9.402  1.00 15.90
ATOM    527  CA  ALA A  78       3.071  -4.577  10.073  1.00 19.47
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ATOM	528	C	ALA	A	78	4.381	-4.332	10.819	1.00	24.48
ATOM	529	O	ALA	A	78	4.389	-4.729	11.983	1.00	26.91
ATOM	530	CB	ALA	A	78	3.390	-5.808	9.336	1.00	17.23
ATOM	531	N	ASN	A	79	5.350	-3.863	10.093	1.00	21.58
ATOM	532	CA	ASN	A	79	6.602	-3.576	10.774	1.00	20.62
ATOM	533	C	ASN	A	79	6.480	-2.673	11.969	1.00	20.93
ATOM	534	O	ASN	A	79	6.975	-2.944	13.053	1.00	15.52
ATOM	535	CB	ASN	A	79	7.474	-3.069	9.670	1.00	24.79
ATOM	536	CG	ASN	A	79	7.933	-4.238	8.824	1.00	28.76
ATOM	537	OD1	ASN	A	79	7.867	-5.439	9.091	1.00	25.30
ATOM	538	ND2	ASN	A	79	8.488	-3.891	7.660	1.00	24.90
ATOM	539	N	ILE	A	80	5.731	-1.611	11.936	1.00	15.93
ATOM	540	CA	ILE	A	80	5.586	-0.574	12.924	1.00	17.00
ATOM	541	C	ILE	A	80	4.925	-1.187	14.118	1.00	20.63
ATOM	542	O	ILE	A	80	5.234	-0.939	15.264	1.00	18.79
ATOM	543	CB	ILE	A	80	4.756	0.629	12.436	1.00	11.98
ATOM	544	CG1	ILE	A	80	5.627	1.124	11.297	1.00	9.50
ATOM	545	CG2	ILE	A	80	4.379	1.728	13.354	1.00	16.27
ATOM	546	CD1	ILE	A	80	5.007	2.071	10.424	1.00	8.15
ATOM	547	N	ASP	A	81	4.017	-2.019	13.708	1.00	19.21
ATOM	548	CA	ASP	A	81	3.304	-2.778	14.728	1.00	15.15
ATOM	549	C	ASP	A	81	4.147	-3.711	15.510	1.00	15.77
ATOM	550	O	ASP	A	81	4.084	-3.697	16.695	1.00	15.82
ATOM	551	CB	ASP	A	81	2.291	-3.438	13.868	1.00	26.36
ATOM	552	CG	ASP	A	81	1.065	-2.530	13.790	1.00	23.71
ATOM	553	OD1	ASP	A	81	1.105	-1.355	14.226	1.00	14.33
ATOM	554	OD2	ASP	A	81	0.061	-3.125	13.222	1.00	33.05
ATOM	555	N	GLU	A	82	5.148	-4.447	15.096	1.00	16.07
ATOM	556	CA	GLU	A	82	5.984	-5.318	15.882	1.00	14.77
ATOM	557	C	GLU	A	82	6.839	-4.355	16.667	1.00	19.33
ATOM	558	O	GLU	A	82	7.315	-4.708	17.752	1.00	23.58
ATOM	559	CB	GLU	A	82	6.998	-6.031	15.064	1.00	13.20
ATOM	560	CG	GLU	A	82	7.792	-7.239	15.476	1.00	23.09
ATOM	561	CD	GLU	A	82	6.767	-8.114	16.185	1.00	29.68
ATOM	562	OE1	GLU	A	82	5.666	-7.670	16.403	1.00	26.63
ATOM	563	OE2	GLU	A	82	7.273	-9.181	16.411	1.00	33.08
ATOM	564	N	GLY	A	83	7.228	-3.227	16.199	1.00	16.79
ATOM	565	CA	GLY	A	83	8.033	-2.428	17.140	1.00	17.32
ATOM	566	C	GLY	A	83	7.238	-2.018	18.366	1.00	17.54
ATOM	567	O	GLY	A	83	7.561	-2.103	19.528	1.00	15.06
ATOM	568	N	LYS	A	84	6.093	-1.408	18.114	1.00	18.72
ATOM	569	CA	LYS	A	84	5.050	-1.146	19.096	1.00	16.90
ATOM	570	C	LYS	A	84	4.893	-2.337	20.057	1.00	17.74
ATOM	571	O	LYS	A	84	4.962	-2.265	21.295	1.00	14.31
ATOM	572	CB	LYS	A	84	3.799	-0.872	18.307	1.00	14.62
ATOM	573	CG	LYS	A	84	3.535	0.565	18.291	1.00	19.30
ATOM	574	CD	LYS	A	84	2.787	1.013	17.044	1.00	34.24
ATOM	575	CE	LYS	A	84	1.568	1.902	17.337	1.00	37.70
ATOM	576	NZ	LYS	A	84	0.346	1.226	16.827	1.00	48.42
ATOM	577	N	ARG	A	85	4.617	-3.506	19.519	1.00	18.50
ATOM	578	CA	ARG	A	85	4.583	-4.705	20.280	1.00	19.04
ATOM	579	C	ARG	A	85	5.677	-4.733	21.308	1.00	19.63
ATOM	580	O	ARG	A	85	5.442	-5.192	22.383	1.00	19.24

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ATOM    581  CB  ARG A  85       4.740  -5.979  19.464  1.00 14.74
ATOM    582  CG  ARG A  85       3.843  -7.094  19.887  1.00  8.85
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ATOM    584  NE  ARG A  85       5.483  -8.898  19.194  1.00 20.30
ATOM    585  CZ  ARG A  85       6.170  -9.705  19.899  1.00 18.19
ATOM    586  NH1 ARG A  85       5.627 -10.161  21.040  1.00 34.03
ATOM    587  NH2 ARG A  85       7.345  -9.979  19.555  1.00 15.36
ATOM    588  N   LEU A  86       6.901  -4.586  20.956  1.00 22.21
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ATOM    590  C   LEU A  86       8.044  -3.637  22.803  1.00 20.73
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ATOM    595  CD2 LEU A  86       9.362  -7.516  21.020  1.00  5.17
ATOM    596  N   PHE A  87       7.700  -2.446  22.529  1.00 16.79
ATOM    597  CA  PHE A  87       7.850  -1.416  23.492  1.00 18.21
ATOM    598  C   PHE A  87       6.939  -1.805  24.618  1.00 26.51
ATOM    599  O   PHE A  87       7.082  -1.565  25.839  1.00 30.36
ATOM    600  CB  PHE A  87       7.498  -0.118  22.846  1.00 15.81
ATOM    601  CG  PHE A  87       8.661   0.503  22.128  1.00 22.72
ATOM    602  CD1 PHE A  87       9.625   1.163  22.795  1.00 25.90
ATOM    603  CD2 PHE A  87       8.800   0.446  20.774  1.00 24.19
ATOM    604  CE1 PHE A  87      10.699   1.781  22.220  1.00 26.46
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ATOM    613  CA  LEU A  89       6.188  -6.032  26.208  1.00 19.29
ATOM    614  C   LEU A  89       7.250  -5.507  27.133  1.00 22.06
ATOM    615  O   LEU A  89       7.449  -6.050  28.177  1.00 20.49
ATOM    616  CB  LEU A  89       7.021  -6.863  25.221  1.00 18.41
ATOM    617  CG  LEU A  89       7.477  -8.167  25.834  1.00 20.45
ATOM    618  CD1 LEU A  89       6.326  -8.707  26.627  1.00 17.22
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ATOM	636	O	GLN	A	92	5.227	-6.519	32.440	1.00	39.47
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ATOM	638	CG	GLN	A	92	2.689	-6.698	30.142	1.00	78.63
ATOM	639	CD	GLN	A	92	2.806	-8.167	29.805	1.00	93.87
ATOM	640	OE1	GLN	A	92	3.597	-8.840	30.475	1.00	96.99
ATOM	641	NE2	GLN	A	92	2.083	-8.696	28.824	1.00	97.81
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ATOM	643	CA	LYS	A	93	7.675	-7.204	31.972	1.00	25.22
ATOM	644	C	LYS	A	93	8.381	-6.298	33.015	1.00	24.68
ATOM	645	O	LYS	A	93	8.716	-6.793	34.075	1.00	32.13
ATOM	646	CB	LYS	A	93	8.673	-7.980	31.148	1.00	10.86
ATOM	647	CG	LYS	A	93	8.225	-8.963	30.159	1.00	24.26
ATOM	648	CD	LYS	A	93	9.362	-9.966	29.986	1.00	21.96
ATOM	649	CE	LYS	A	93	9.093	-10.718	28.658	1.00	23.78
ATOM	650	NZ	LYS	A	93	10.084	-11.805	28.300	1.00	25.87
ATOM	651	N	CYS	A	94	8.752	-5.096	32.774	1.00	16.62
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ATOM	655	CB	CYS	A	94	11.147	-4.691	32.911	1.00	3.14
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ATOM	677	OG1	THR	A	97	14.602	-1.915	32.528	1.00	38.91
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ATOM	691	CG1	VAL	A	99	12.666	1.272	25.872	1.00	17.40
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ATOM	695	C	VAL	A	100	16.389	2.159	23.561	1.00	10.79
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ATOM	698	CG1	VAL	A	100	17.824	4.252	26.336	1.00	6.05
ATOM	699	CG2	VAL	A	100	18.853	2.053	25.591	1.00	6.68
ATOM	700	N	ALA	A	101	16.277	2.928	22.511	1.00	13.14
ATOM	701	CA	ALA	A	101	16.127	2.266	21.183	1.00	15.67
ATOM	702	C	ALA	A	101	17.065	2.747	20.053	1.00	12.08
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ATOM	709	N	GLY	A	103	17.706	2.407	15.648	1.00	7.80
ATOM	710	CA	GLY	A	103	17.446	1.745	14.356	1.00	5.33
ATOM	711	C	GLY	A	103	18.303	2.211	13.180	1.00	7.56
ATOM	712	O	GLY	A	103	18.785	3.340	13.227	1.00	6.88
ATOM	713	N	TYR	A	104	18.490	1.387	12.139	1.00	7.09
ATOM	714	CA	TYR	A	104	19.392	1.682	11.069	1.00	5.99
ATOM	715	C	TYR	A	104	18.705	1.614	9.705	1.00	9.47
ATOM	716	O	TYR	A	104	18.115	0.638	9.441	1.00	6.46
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ATOM	718	CG	TYR	A	104	21.436	1.078	9.876	1.00	8.05
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ATOM	720	CD2	TYR	A	104	21.961	-0.044	9.172	1.00	6.85
ATOM	721	CE1	TYR	A	104	22.447	2.513	8.186	1.00	5.61
ATOM	722	CE2	TYR	A	104	22.751	0.052	8.072	1.00	7.49
ATOM	723	CZ	TYR	A	104	22.972	1.377	7.608	1.00	11.08
ATOM	724	OH	TYR	A	104	23.795	1.509	6.479	1.00	14.32
ATOM	725	N	SER	A	105	18.939	2.975	8.852	1.00	18.39
ATOM	726	CA	SER	A	105	18.190	2.854	7.601	1.00	9.66
ATOM	727	C	SER	A	105	16.763	2.370	7.722	1.00	6.10
ATOM	728	O	SER	A	105	16.090	3.304	8.077	1.00	5.63
ATOM	729	CB	SER	A	105	19.124	2.159	6.607	1.00	8.55
ATOM	730	OG	SER	A	105	18.553	1.685	5.463	1.00	24.30
ATOM	731	N	GLN	A	106	16.241	1.405	7.079	1.00	9.93
ATOM	732	CA	GLN	A	106	14.759	1.316	7.002	1.00	8.25
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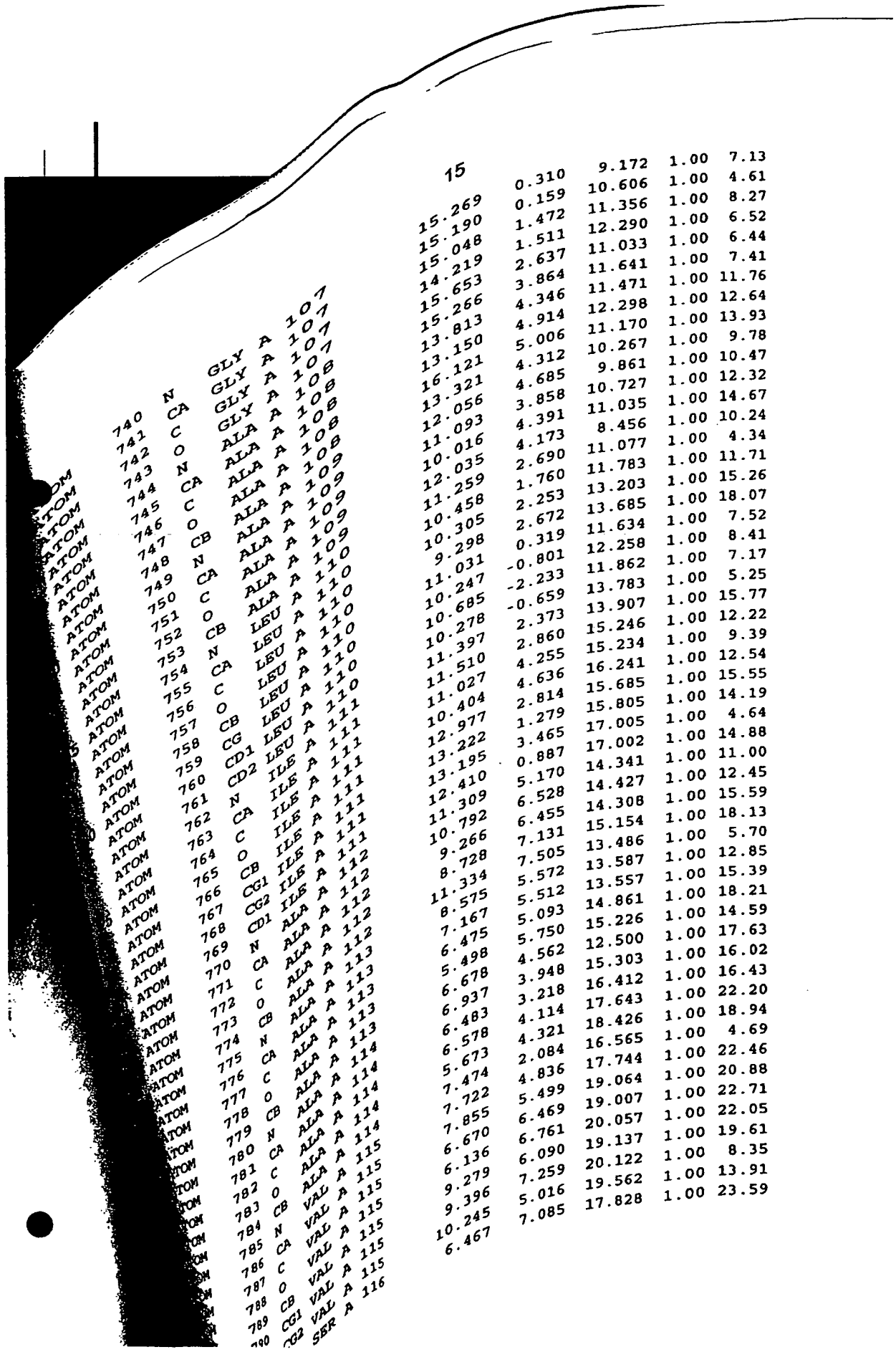
ATOM	737	CD	GLN	A	106	12.228	-1.220	5.581	1.00	16.87
ATOM	738	OE1	GLN	A	106	11.024	-1.180	5.492	1.00	17.59
ATOM	739	NE2	GLN	A	106	12.643	-2.032	4.713	1.00	8.32



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795	O	SER	A	116	3.333	8.523	18.399	1.00 27.35
796	CB	SER	A	116	5.522	8.865	16.376	1.00 25.21
797	OG	SER	A	116	5.168	8.043	15.277	1.00 28.05
798	N	GLU	A	117	3.859	6.397	18.004	1.00 18.83
799	CA	GLU	A	117	2.491	6.020	18.238	1.00 22.21
800	C	GLU	A	117	2.461	5.474	19.653	1.00 30.46
801	O	GLU	A	117	1.487	4.773	19.863	1.00 35.72
802	CB	GLU	A	117	1.977	4.902	17.343	1.00 21.63
803	CG	GLU	A	117	2.167	5.219	15.897	1.00 26.41
804	CD	GLU	A	117	1.560	4.424	14.814	1.00 34.01
805	OE1	GLU	A	117	0.912	3.440	15.046	1.00 32.59
806	OE2	GLU	A	117	1.750	4.833	13.659	1.00 44.62
807	N	LEU	A	118	3.438	5.570	20.512	1.00 34.45
808	CA	LEU	A	118	3.326	5.006	21.812	1.00 33.64
809	C	LEU	A	118	2.681	6.110	22.633	1.00 41.75
810	O	LEU	A	118	2.594	7.267	22.370	1.00 39.90
811	CB	LEU	A	118	4.600	4.668	22.392	1.00 29.44
812	CG	LEU	A	118	5.628	3.891	21.645	1.00 26.36
813	CD1	LEU	A	118	6.921	3.840	22.379	1.00 27.53
814	CD2	LEU	A	118	5.110	2.520	21.536	1.00 20.69
815	N	SER	A	119	2.076	5.794	23.726	1.00 48.86
816	CA	SER	A	119	0.910	5.647	24.476	1.00 52.44
817	C	SER	A	119	1.212	6.063	25.866	1.00 52.57
818	O	SER	A	119	1.485.	5.258	26.735	1.00 55.54
819	CB	SER	A	119	0.550	4.132	24.488	1.00 70.55
820	OG	SER	A	119	1.393	3.091	23.908	1.00 66.80
821	N	GLY	A	120	1.532	7.307	26.024	1.00 52.95
822	CA	GLY	A	120	1.910	7.761	27.382	1.00 53.35
823	C	GLY	A	120	2.944	7.109	28.291	1.00 49.09
824	O	GLY	A	120	4.086	7.617	28.358	1.00 49.66
825	N	ALA	A	121	2.526	6.129	29.102	1.00 42.97
826	CA	ALA	A	121	3.477	5.574	30.022	1.00 40.72
827	C	ALA	A	121	4.587	4.772	29.326	1.00 44.20
828	O	ALA	A	121	5.749	4.803	29.711	1.00 45.42
829	CB	ALA	A	121	2.965	4.542	30.903	1.00 36.34
830	N	VAL	A	122	4.122	4.035	28.312	1.00 41.15
831	CA	VAL	A	122	5.090	3.269	27.548	1.00 33.41
832	C	VAL	A	122	5.870	4.168	26.652	1.00 28.48
833	O	VAL	A	122	7.084	4.019	26.872	1.00 27.69
834	CB	VAL	A	122	4.424	2.056	26.952	1.00 30.22
835	CG1	VAL	A	122	2.924	1.997	27.098	1.00 28.03
836	CG2	VAL	A	122	4.891	1.836	25.551	1.00 23.22
837	N	LYS	A	123	5.424	5.310	26.177	1.00 23.16
838	CA	LYS	A	123	6.354	6.314	25.661	1.00 23.11
839	C	LYS	A	123	7.403	6.783	26.661	1.00 25.28
840	O	LYS	A	123	8.524	7.224	26.449	1.00 29.01
841	CB	LYS	A	123	5.561	7.502	25.100	1.00 23.54
842	CG	LYS	A	123	6.171	8.573	24.277	1.00 26.71
843	CD	LYS	A	123	5.400	9.775	23.888	1.00 43.07
844	CE	LYS	A	123	4.953	9.783	22.461	1.00 59.59
845	NZ	LYS	A	123	3.518	9.637	22.099	1.00 67.50

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ATOM    846  N   GLU A 124       6.977   6.991  27.918  1.00 27.95
ATOM    847  CA  GLU A 124       7.845   7.700  28.863  1.00 27.29
ATOM    848  C   GLU A 124       8.910   6.706  29.243  1.00 25.21
ATOM    849  O   GLU A 124       9.993   7.165  29.769  1.00 21.21
ATOM    850  CB  GLU A 124       6.986   8.351  29.927  1.00 40.13
ATOM    851  CG  GLU A 124       7.588   8.609  31.295  1.00 57.40
ATOM    852  CD  GLU A 124       8.530   9.814  31.247  1.00 66.99
ATOM    853  OE1 GLU A 124       9.619   9.751  31.902  1.00 70.44
ATOM    854  OE2 GLU A 124       7.949  10.652  30.502  1.00 73.84
ATOM    855  N   GLN A 125       8.656   5.393  29.058  1.00 19.93
ATOM    856  CA  GLN A 125       9.761   4.509  29.546  1.00 17.98
ATOM    857  C   GLN A 125      10.865   4.556  28.521  1.00 24.28
ATOM    858  O   GLN A 125      11.964   4.107  28.815  1.00 21.47
ATOM    859  CB  GLN A 125       9.225   3.178  29.844  1.00  9.13
ATOM    860  CG  GLN A 125       9.901   2.001  30.299  1.00  9.05
ATOM    861  CD  GLN A 125       9.211   0.719  30.129  1.00 19.33
ATOM    862  OE1 GLN A 125       8.190   0.703  29.466  1.00 28.52
ATOM    863  NE2 GLN A 125       9.662  -0.396  30.684  1.00 13.34
ATOM    864  N   VAL A 126      10.593   5.188  27.319  1.00 25.30
ATOM    865  CA  VAL A 126      11.738   5.124  26.361  1.00 22.55
ATOM    866  C   VAL A 126      12.546   6.334  26.614  1.00 17.55
ATOM    867  O   VAL A 126      12.109   7.408  26.329  1.00 12.79
ATOM    868  CB  VAL A 126      11.227   4.560  25.022  1.00 23.76
ATOM    869  CG1 VAL A 126       9.706   4.686  24.946  1.00 23.77
ATOM    870  CG2 VAL A 126      11.795   5.081  23.743  1.00 23.81
ATOM    871  N   LYS A 127      13.726   6.233  27.264  1.00 16.41
ATOM    872  CA  LYS A 127      14.462   7.494  27.639  1.00 18.18
ATOM    873  C   LYS A 127      15.239   8.063  26.488  1.00 18.49
ATOM    874  O   LYS A 127      15.812   9.103  26.680  1.00 18.99
ATOM    875  CB  LYS A 127      15.401   7.148  28.792  1.00 20.81
ATOM    876  CG  LYS A 127      14.770   6.110  29.713  1.00 21.99
ATOM    877  CD  LYS A 127      13.435   6.726  30.064  1.00 33.86
ATOM    878  CE  LYS A 127      12.779   6.612  31.399  1.00 32.17
ATOM    879  NZ  LYS A 127      12.279   7.863  31.993  1.00 45.34
ATOM    880  N   GLY A 128      15.522   7.281  25.416  1.00 20.56
ATOM    881  CA  GLY A 128      16.280   7.948  24.306  1.00 20.72
ATOM    882  C   GLY A 128      16.358   7.104  23.063  1.00 17.71
ATOM    883  O   GLY A 128      16.168   5.901  23.226  1.00 16.66
ATOM    884  N   VAL A 129      16.451   7.725  21.892  1.00 16.16
ATOM    885  CA  VAL A 129      16.497   6.872  20.691  1.00 13.82
ATOM    886  C   VAL A 129      17.519   7.371  19.719  1.00  8.35
ATOM    887  O   VAL A 129      17.602   8.553  19.556  1.00  3.85
ATOM    888  CB  VAL A 129      15.192   6.426  20.054  1.00 11.02
ATOM    889  CG1 VAL A 129      14.007   7.041  20.726  1.00  6.50
ATOM    890  CG2 VAL A 129      15.051   6.729  18.571  1.00 10.03
ATOM    891  N   ALA A 130      18.455   6.398  19.363  1.00  8.05
ATOM    892  CA  ALA A 130      19.430   6.845  18.344  1.00  7.55
ATOM    893  C   ALA A 130      19.078   6.293  16.958  1.00 11.17
ATOM    894  O   ALA A 130      18.755   5.145  16.849  1.00 15.74
ATOM    895  CB  ALA A 130      20.781   6.391  18.603  1.00  5.89
ATOM    896  N   LEU A 131      18.911   6.953  15.892  1.00  7.36
ATOM    897  CA  LEU A 131      18.635   6.625  14.553  1.00  7.70
ATOM    898  C   LEU A 131      19.876   6.908  13.661  1.00 12.02
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ATOM	899	O	LEU	A	131	20.436	8.033	13.604	1.00	6.80
ATOM	900	CB	LEU	A	131	17.604	7.713	14.102	1.00	8.40
ATOM	901	CG	LEU	A	131	16.160	7.830	14.575	1.00	6.67
ATOM	902	CD1	LEU	A	131	15.391	8.957	13.981	1.00	4.49
ATOM	903	CD2	LEU	A	131	15.481	6.488	14.324	1.00	5.12
ATOM	904	N	PHE	A	132	20.271	6.009	12.802	1.00	11.56
ATOM	905	CA	PHE	A	132	21.422	6.183	11.908	1.00	10.44
ATOM	906	C	PHE	A	132	20.965	6.013	10.478	1.00	8.46
ATOM	907	O	PHE	A	132	20.175	5.101	10.097	1.00	11.04
ATOM	908	CB	PHE	A	132	22.217	4.931	12.282	1.00	10.56
ATOM	909	CG	PHE	A	132	22.693	4.830	13.714	1.00	16.38
ATOM	910	CD1	PHE	A	132	21.951	4.029	14.542	1.00	13.36
ATOM	911	CD2	PHE	A	132	23.860	5.489	14.213	1.00	15.12
ATOM	912	CE1	PHE	A	132	22.342	3.911	15.889	1.00	14.91
ATOM	913	CE2	PHE	A	132	24.176	5.323	15.513	1.00	18.02
ATOM	914	CZ	PHE	A	132	23.426	4.530	16.403	1.00	15.09
ATOM	915	N	GLY	A	133	21.431	6.876	9.580	1.00	7.35
ATOM	916	CA	GLY	A	133	21.026	6.893	8.148	1.00	5.86
ATOM	917	C	GLY	A	133	19.503	6.919	8.061	1.00	12.25
ATOM	918	O	GLY	A	133	18.890	5.926	7.593	1.00	9.03
ATOM	919	N	TYR	A	134	18.926	8.070	8.532	1.00	9.85
ATOM	920	CA	TYR	A	134	17.455	8.022	8.838	1.00	7.40
ATOM	921	C	TYR	A	134	16.647	8.365	7.584	1.00	10.61
ATOM	922	O	TYR	A	134	16.785	9.513	7.131	1.00	5.85
ATOM	923	CB	TYR	A	134	17.161	9.128	9.836	1.00	7.27
ATOM	924	CG	TYR	A	134	15.842	9.393	10.391	1.00	7.89
ATOM	925	CD1	TYR	A	134	14.889	8.437	10.312	1.00	6.65
ATOM	926	CD2	TYR	A	134	15.661	10.651	10.948	1.00	11.44
ATOM	927	CE1	TYR	A	134	13.657	8.690	10.821	1.00	9.05
ATOM	928	CE2	TYR	A	134	14.408	10.928	11.467	1.00	12.89
ATOM	929	CZ	TYR	A	134	13.428	9.923	11.423	1.00	14.22
ATOM	930	OH	TYR	A	134	12.146	10.110	11.975	1.00	12.41
ATOM	931	N	THR	A	135	15.811	7.398	7.139	1.00	11.51
ATOM	932	CA	THR	A	135	15.229	7.581	5.789	1.00	7.71
ATOM	933	C	THR	A	135	14.082	8.530	5.825	1.00	10.36
ATOM	934	O	THR	A	135	13.845	8.878	4.727	1.00	11.26
ATOM	935	CB	THR	A	135	14.772	6.394	4.967	1.00	12.02
ATOM	936	OG1	THR	A	135	13.821	5.399	5.398	1.00	22.81
ATOM	937	CG2	THR	A	135	15.828	5.332	4.712	1.00	14.88
ATOM	938	N	GLN	A	136	13.632	9.105	6.928	1.00	15.28
ATOM	939	CA	GLN	A	136	12.596	10.134	6.968	1.00	16.48
ATOM	940	C	GLN	A	136	13.102	11.418	7.646	1.00	17.46
ATOM	941	O	GLN	A	136	12.292	12.231	8.035	1.00	12.82
ATOM	942	CB	GLN	A	136	11.336	9.671	7.701	1.00	5.71
ATOM	943	CG	GLN	A	136	11.178	8.191	7.263	1.00	13.60
ATOM	944	CD	GLN	A	136	10.504	8.264	5.932	1.00	14.65
ATOM	945	OE1	GLN	A	136	9.587	9.102	5.986	1.00	23.99
ATOM	946	NE2	GLN	A	136	10.852	7.529	4.914	1.00	14.68
ATOM	947	N	ASN	A	137	14.421	11.532	7.566	1.00	18.52
ATOM	948	CA	ASN	A	137	14.953	12.752	8.141	1.00	18.16
ATOM	949	C	ASN	A	137	14.301	13.929	7.458	1.00	19.79
ATOM	950	O	ASN	A	137	13.895	14.802	8.157	1.00	12.28
ATOM	951	CB	ASN	A	137	16.481	12.573	8.239	1.00	14.17

ATOM	952	CG	ASN	A	137	17.247	13.740	8.812	1.00	19.75
ATOM	953	OD1	ASN	A	137	17.821	14.341	7.934	1.00	14.52
ATOM	954	ND2	ASN	A	137	17.390	14.130	10.042	1.00	17.43
ATOM	955	N	LEU	A	138	14.180	14.062	6.141	1.00	27.31
ATOM	956	CA	LEU	A	138	13.640	15.270	5.553	1.00	25.53
ATOM	957	C	LEU	A	138	12.190	15.332	5.971	1.00	22.45
ATOM	958	O	LEU	A	138	11.710	16.281	6.549	1.00	25.13
ATOM	959	CB	LEU	A	138	13.632	15.269	4.056	1.00	41.28
ATOM	960	CG	LEU	A	138	13.713	16.582	3.303	1.00	31.76
ATOM	961	CD1	LEU	A	138	14.641	17.503	4.012	1.00	51.09
ATOM	962	CD2	LEU	A	138	14.207	16.573	1.958	1.00	46.20
ATOM	963	N	GLN	A	139	11.378	14.403	5.569	1.00	20.48
ATOM	964	CA	GLN	A	139	10.034	14.390	6.037	1.00	19.98
ATOM	965	C	GLN	A	139	9.846	14.749	7.471	1.00	22.85
ATOM	966	O	GLN	A	139	8.791	15.282	7.528	1.00	26.66
ATOM	967	CB	GLN	A	139	9.517	12.969	5.899	1.00	18.37
ATOM	968	CG	GLN	A	139	9.684	12.643	4.450	1.00	22.02
ATOM	969	CD	GLN	A	139	10.984	11.983	4.110	1.00	22.69
ATOM	970	OE1	GLN	A	139	10.674	10.980	3.477	1.00	35.62
ATOM	971	NE2	GLN	A	139	12.195	12.405	4.410	1.00	31.70
ATOM	972	N	ASN	A	140	10.454	14.072	8.427	1.00	26.14
ATOM	973	CA	ASN	A	140	10.215	14.183	9.848	1.00	19.06
ATOM	974	C	ASN	A	140	10.941	15.429	10.293	1.00	16.99
ATOM	975	O	ASN	A	140	11.040	15.654	11.454	1.00	18.05
ATOM	976	CB	ASN	A	140	10.581	12.910	10.541	1.00	17.20
ATOM	977	CG	ASN	A	140	9.465	11.998	10.210	1.00	16.28
ATOM	978	OD1	ASN	A	140	8.615	12.565	9.563	1.00	23.57
ATOM	979	ND2	ASN	A	140	9.460	10.756	10.630	1.00	22.65
ATOM	980	N	ARG	A	141	11.457	16.162	9.397	1.00	19.20
ATOM	981	CA	ARG	A	141	12.170	17.350	9.790	1.00	26.25
ATOM	982	C	ARG	A	141	13.219	17.090	10.818	1.00	25.06
ATOM	983	O	ARG	A	141	13.365	17.928	11.649	1.00	27.60
ATOM	984	CB	ARG	A	141	11.123	18.299	10.271	1.00	37.72
ATOM	985	CG	ARG	A	141	10.083	18.974	9.372	1.00	49.61
ATOM	986	N	GLY	A	142	14.110	16.165	10.920	1.00	19.42
ATOM	987	CA	GLY	A	142	14.997	15.778	11.902	1.00	14.21
ATOM	988	C	GLY	A	142	14.652	15.066	13.158	1.00	19.42
ATOM	989	O	GLY	A	142	15.547	14.759	13.971	1.00	23.74
ATOM	990	N	GLY	A	143	13.354	14.851	13.569	1.00	14.09
ATOM	991	CA	GLY	A	143	13.210	14.075	14.757	1.00	11.80
ATOM	992	C	GLY	A	143	12.203	12.972	14.555	1.00	16.69
ATOM	993	O	GLY	A	143	11.760	12.787	13.481	1.00	19.57
ATOM	994	N	ILE	A	144	11.668	12.386	15.590	1.00	19.71
ATOM	995	CA	ILE	A	144	10.494	11.589	15.667	1.00	20.13
ATOM	996	C	ILE	A	144	9.313	12.315	16.296	1.00	27.00
ATOM	997	O	ILE	A	144	9.298	13.026	17.268	1.00	26.75
ATOM	998	CB	ILE	A	144	10.973	10.583	16.692	1.00	16.84
ATOM	999	CG1	ILE	A	144	12.363	9.956	16.348	1.00	5.60
ATOM	1000	CG2	ILE	A	144	9.882	9.636	16.775	1.00	14.01
ATOM	1001	CD1	ILE	A	144	12.437	9.156	17.562	1.00	2.75
ATOM	1002	N	PRO	A	145	8.249	12.380	15.499	1.00	32.77
ATOM	1003	CA	PRO	A	145	6.959	12.993	15.779	1.00	29.89
ATOM	1004	C	PRO	A	145	6.484	12.588	17.180	1.00	27.78

ATOM	1005	O	PRO	A	145	6.475	11.446	17.537	1.00 26.07
ATOM	1006	CB	PRO	A	145	5.957	12.384	14.784	1.00 26.51
ATOM	1007	CG	PRO	A	145	6.887	12.059	13.668	1.00 25.85
ATOM	1008	CD	PRO	A	145	8.174	11.563	14.234	1.00 31.33
ATOM	1009	N	ASN	A	146	5.796	13.462	17.878	1.00 27.07
ATOM	1010	CA	ASN	A	146	5.454	13.274	19.230	1.00 28.59
ATOM	1011	C	ASN	A	146	6.526	12.605	20.045	1.00 29.25
ATOM	1012	O	ASN	A	146	6.087	11.995	20.996	1.00 35.51
ATOM	1013	CB	ASN	A	146	4.285	12.364	19.230	1.00 41.13
ATOM	1014	CG	ASN	A	146	3.300	12.568	18.120	1.00 48.43
ATOM	1015	OD1	ASN	A	146	3.134	13.721	17.788	1.00 49.24
ATOM	1016	ND2	ASN	A	146	2.763	11.437	17.695	1.00 47.79
ATOM	1017	N	TYR	A	147	7.791	12.799	19.885	1.00 23.88
ATOM	1018	CA	TYR	A	147	8.689	12.339	20.969	1.00 21.90
ATOM	1019	C	TYR	A	147	9.583	13.495	21.285	1.00 22.57
ATOM	1020	O	TYR	A	147	9.777	14.399	20.494	1.00 26.53
ATOM	1021	CB	TYR	A	147	9.309	11.098	20.498	1.00 21.16
ATOM	1022	CG	TYR	A	147	10.285	10.471	21.349	1.00 20.45
ATOM	1023	CD1	TYR	A	147	9.882	9.720	22.384	1.00 24.28
ATOM	1024	CD2	TYR	A	147	11.608	10.564	21.189	1.00 17.96
ATOM	1025	CE1	TYR	A	147	10.681	9.029	23.273	1.00 24.55
ATOM	1026	CE2	TYR	A	147	12.509	9.948	21.983	1.00 20.73
ATOM	1027	CZ	TYR	A	147	12.022	9.184	23.030	1.00 24.61
ATOM	1028	OH	TYR	A	147	12.891	8.536	23.887	1.00 24.80
ATOM	1029	N	PRO	A	148	9.893	13.858	22.507	1.00 22.86
ATOM	1030	CA	PRO	A	148	10.817	14.916	22.769	1.00 21.77
ATOM	1031	C	PRO	A	148	12.127	14.882	21.957	1.00 22.49
ATOM	1032	O	PRO	A	148	13.007	14.004	22.117	1.00 22.31
ATOM	1033	CB	PRO	A	148	11.185	14.694	24.251	1.00 23.23
ATOM	1034	CG	PRO	A	148	10.324	13.576	24.719	1.00 23.39
ATOM	1035	CD	PRO	A	148	9.677	12.889	23.590	1.00 25.33
ATOM	1036	N	ARG	A	149	12.432	15.980	21.250	1.00 25.45
ATOM	1037	CA	ARG	A	149	13.735	16.138	20.567	1.00 22.54
ATOM	1038	C	ARG	A	149	14.910	16.018	21.499	1.00 21.28
ATOM	1039	O	ARG	A	149	15.860	15.477	21.015	1.00 16.61
ATOM	1040	CB	ARG	A	149	13.829	17.346	19.727	1.00 31.02
ATOM	1041	CG	ARG	A	149	12.837	17.750	18.719	1.00 58.26
ATOM	1042	CD	ARG	A	149	13.452	18.605	17.658	1.00 80.58
ATOM	1043	NE	ARG	A	149	13.769	17.798	16.491	1.00 92.05
ATOM	1044	CZ	ARG	A	149	13.315	18.154	15.320	1.00 91.85
ATOM	1045	NH1	ARG	A	149	12.586	19.213	15.165	1.00 86.98
ATOM	1046	NH2	ARG	A	149	13.544	17.488	14.242	1.00 91.61
ATOM	1047	N	GLU	A	150	14.813	16.282	22.825	1.00 28.09
ATOM	1048	CA	GLU	A	150	15.950	16.171	23.735	1.00 25.55
ATOM	1049	C	GLU	A	150	16.272	14.736	24.020	1.00 21.12
ATOM	1050	O	GLU	A	150	17.372	14.443	24.371	1.00 24.39
ATOM	1051	CB	GLU	A	150	15.753	17.040	24.917	1.00 38.73
ATOM	1052	CG	GLU	A	150	14.328	17.370	25.359	1.00 67.27
ATOM	1053	CD	GLU	A	150	14.252	17.185	26.899	1.00 85.05
ATOM	1054	OE1	GLU	A	150	15.005	17.890	27.657	1.00 90.70
ATOM	1055	OE2	GLU	A	150	13.454	16.321	27.373	1.00 91.68
ATOM	1056	N	ARG	A	151	15.396	13.807	23.727	1.00 19.70
ATOM	1057	CA	ARG	A	151	15.752	12.424	23.844	1.00 19.52

ATOM	1058	C	ARG	A	151	16.163	11.779	22.531	1.00 19.28
ATOM	1059	O	ARG	A	151	16.373	10.586	22.480	1.00 14.55
ATOM	1060	CB	ARG	A	151	14.548	11.796	24.412	1.00 23.06
ATOM	1061	CG	ARG	A	151	13.853	12.432	25.516	1.00 22.24
ATOM	1062	CD	ARG	A	151	13.200	11.451	26.393	1.00 33.40
ATOM	1063	NE	ARG	A	151	12.609	11.893	27.633	1.00 46.53
ATOM	1064	CZ	ARG	A	151	11.796	11.028	28.275	1.00 52.87
ATOM	1065	NH1	ARG	A	151	11.428	9.823	27.930	1.00 51.02
ATOM	1066	NH2	ARG	A	151	11.203	11.278	29.416	1.00 59.98
ATOM	1067	N	THR	A	152	16.360	12.526	21.505	1.00 14.12
ATOM	1068	CA	THR	A	152	16.629	11.925	20.253	1.00 15.05
ATOM	1069	C	THR	A	152	17.995	12.249	19.745	1.00 17.30
ATOM	1070	O	THR	A	152	18.282	13.373	19.965	1.00 21.34
ATOM	1071	CB	THR	A	152	15.680	12.408	19.158	1.00 13.91
ATOM	1072	OG1	THR	A	152	14.423	12.256	19.858	1.00 23.92
ATOM	1073	CG2	THR	A	152	15.737	11.934	17.759	1.00 6.77
ATOM	1074	N	LYS	A	153	18.704	11.336	19.121	1.00 15.49
ATOM	1075	CA	LYS	A	153	19.930	11.725	18.450	1.00 17.73
ATOM	1076	C	LYS	A	153	19.893	11.035	17.073	1.00 18.41
ATOM	1077	O	LYS	A	153	19.866	9.800	17.121	1.00 16.04
ATOM	1078	CB	LYS	A	153	21.112	11.260	19.338	1.00 14.55
ATOM	1079	CG	LYS	A	153	22.523	11.508	18.933	1.00 11.95
ATOM	1080	CD	LYS	A	153	22.883	12.882	19.403	1.00 40.35
ATOM	1081	CE	LYS	A	153	24.358	13.093	19.079	1.00 62.12
ATOM	1082	NZ	LYS	A	153	24.930	14.235	19.863	1.00 73.03
ATOM	1083	N	VAL	A	154	19.910	11.962	16.136	1.00 15.86
ATOM	1084	CA	VAL	A	154	20.031	11.508	14.730	1.00 15.79
ATOM	1085	C	VAL	A	154	21.406	11.481	14.040	1.00 13.11
ATOM	1086	O	VAL	A	154	21.958	12.460	13.675	1.00 13.51
ATOM	1087	CB	VAL	A	154	19.095	12.257	13.674	1.00 5.90
ATOM	1088	CG1	VAL	A	154	19.276	11.765	12.247	1.00 8.45
ATOM	1089	CG2	VAL	A	154	17.672	12.091	14.117	1.00 7.14
ATOM	1090	N	PHE	A	155	22.039	10.448	13.605	1.00 13.75
ATOM	1091	CA	PHE	A	155	23.263	10.473	12.843	1.00 10.67
ATOM	1092	C	PHE	A	155	22.906	10.406	11.402	1.00 11.64
ATOM	1093	O	PHE	A	155	22.505	9.367	10.893	1.00 15.09
ATOM	1094	CB	PHE	A	155	23.955	9.120	13.304	1.00 5.38
ATOM	1095	CG	PHE	A	155	24.396	9.266	14.739	1.00 16.52
ATOM	1096	CD1	PHE	A	155	23.678	8.642	15.696	1.00 23.70
ATOM	1097	CD2	PHE	A	155	25.503	9.950	15.107	1.00 11.27
ATOM	1098	CE1	PHE	A	155	24.037	8.702	17.011	1.00 23.25
ATOM	1099	CE2	PHE	A	155	25.888	9.994	16.372	1.00 7.37
ATOM	1100	CZ	PHE	A	155	25.139	9.384	17.357	1.00 16.13
ATOM	1101	N	CYS	A	156	23.205	11.255	10.511	1.00 12.38
ATOM	1102	CA	CYS	A	156	22.847	11.443	9.114	1.00 11.64
ATOM	1103	C	CYS	A	156	24.057	12.027	8.461	1.00 10.08
ATOM	1104	O	CYS	A	156	24.385	13.174	8.378	1.00 13.73
ATOM	1105	CB	CYS	A	156	21.575	12.391	8.917	1.00 6.30
ATOM	1106	SG	CYS	A	156	20.137	11.470	8.287	1.00 10.60
ATOM	1107	N	ASN	A	157	24.814	11.147	7.918	1.00 16.95
ATOM	1108	CA	ASN	A	157	26.229	11.665	7.576	1.00 19.16
ATOM	1109	C	ASN	A	157	26.197	12.367	6.310	1.00 17.70
ATOM	1110	O	ASN	A	157	25.368	12.330	5.469	1.00 20.91

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ATOM   1111  CB  ASN A 157      27.115  10.714   8.300  1.00 30.34
ATOM   1112  CG  ASN A 157      27.733   9.498   7.932  1.00 34.95
ATOM   1113  OD1 ASN A 157      28.011   8.573   8.606  1.00 44.28
ATOM   1114  ND2 ASN A 157      27.965   9.541   6.660  1.00 54.18
ATOM   1115  N   VAL A 158      26.849  13.501   6.313  1.00 25.65
ATOM   1116  CA  VAL A 158      26.825  14.483   5.192  1.00 28.21
ATOM   1117  C   VAL A 158      26.768  13.893   3.758  1.00 24.85
ATOM   1118  O   VAL A 158      25.732  14.266   3.111  1.00 30.96
ATOM   1119  CB  VAL A 158      27.954  15.512   5.217  1.00 27.87
ATOM   1120  CG1 VAL A 158      28.751  14.595   4.238  1.00 40.51
ATOM   1121  CG2 VAL A 158      27.791  16.704   4.399  1.00 34.39
ATOM   1122  N   GLY A 159      27.483  12.956   3.016  1.00  5.94
ATOM   1123  CA  GLY A 159      26.713  12.774   1.732  1.00  6.20
ATOM   1124  C   GLY A 159      25.734  11.797   1.487  1.00  4.00
ATOM   1125  O   GLY A 159      25.732  10.704   0.848  1.00  4.06
ATOM   1126  N   ASP A 160      25.052  11.441   2.643  1.00  8.53
ATOM   1127  CA  ASP A 160      24.106  10.302   2.828  1.00 11.97
ATOM   1128  C   ASP A 160      22.755  10.698   2.177  1.00 14.44
ATOM   1129  O   ASP A 160      21.928  11.398   2.692  1.00 10.21
ATOM   1130  CB  ASP A 160      24.037   9.829   4.277  1.00 12.43
ATOM   1131  CG  ASP A 160      23.126   8.629   4.261  1.00 20.99
ATOM   1132  OD1 ASP A 160      22.525   8.408   3.179  1.00 33.03
ATOM   1133  OD2 ASP A 160      22.956   7.840   5.216  1.00 10.13
ATOM   1134  N   ALA A 161      22.455  10.402   0.961  1.00 12.33
ATOM   1135  CA  ALA A 161      21.318  10.743   0.269  1.00 11.01
ATOM   1136  C   ALA A 161      19.961  10.317   0.848  1.00 15.22
ATOM   1137  O   ALA A 161      18.969  11.034   0.594  1.00  9.50
ATOM   1138  CB  ALA A 161      21.365  10.334  -1.172  1.00 13.68
ATOM   1139  N   VAL A 162      19.915   9.468   1.840  1.00 14.54
ATOM   1140  CA  VAL A 162      18.653   9.014   2.287  1.00  9.86
ATOM   1141  C   VAL A 162      18.235  10.063   3.258  1.00 13.50
ATOM   1142  O   VAL A 162      17.094  10.458   3.377  1.00 20.47
ATOM   1143  CB  VAL A 162      18.596   7.778   3.117  1.00  7.34
ATOM   1144  CG1 VAL A 162      18.931   6.592   2.259  1.00  6.50
ATOM   1145  CG2 VAL A 162      19.514   7.858   4.210  1.00 18.46
ATOM   1146  N   CYS A 163      19.198  10.733   3.719  1.00 13.44
ATOM   1147  CA  CYS A 163      18.864  11.811   4.720  1.00 11.26
ATOM   1148  C   CYS A 163      18.256  12.963   4.042  1.00 15.57
ATOM   1149  O   CYS A 163      18.219  13.857   4.880  1.00 14.09
ATOM   1150  CB  CYS A 163      20.144  12.145   5.570  1.00 18.70
ATOM   1151  SG  CYS A 163      20.748  10.705   6.581  1.00 13.38
ATOM   1152  N   THR A 164      18.100  13.014   2.696  1.00 21.82
ATOM   1153  CA  THR A 164      17.603  14.283   2.171  1.00 23.08
ATOM   1154  C   THR A 164      16.597  14.022   1.098  1.00 23.39
ATOM   1155  O   THR A 164      16.517  14.727   0.137  1.00 33.37
ATOM   1156  CB  THR A 164      18.463  15.341   1.454  1.00 23.25
ATOM   1157  OG1 THR A 164      19.486  14.707   0.674  1.00 23.21
ATOM   1158  CG2 THR A 164      18.958  16.261   2.491  1.00 37.71
ATOM   1159  N   GLY A 165      15.802  13.085   1.309  1.00 24.23
ATOM   1160  CA  GLY A 165      14.606  12.783   0.579  1.00 26.69
ATOM   1161  C   GLY A 165      14.699  11.814  -0.515  1.00 28.56
ATOM   1162  O   GLY A 165      13.680  11.775  -1.124  1.00 39.76
ATOM   1163  N   THR A 166      15.661  11.044  -0.736  1.00 25.80
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ATOM	1164	CA	THR	A	166	16.006	10.220	-1.774	1.00	25.53
ATOM	1165	C	THR	A	166	16.195	8.866	-1.175	1.00	25.35
ATOM	1166	O	THR	A	166	16.913	8.760	-0.206	1.00	30.91
ATOM	1167	CB	THR	A	166	17.406	10.657	-2.230	1.00	31.57
ATOM	1168	OG1	THR	A	166	17.105	11.788	-2.982	1.00	24.13
ATOM	1169	CG2	THR	A	166	18.061	9.559	-2.983	1.00	34.67
ATOM	1170	N	LEU	A	167	15.734	7.833	-1.817	1.00	19.63
ATOM	1171	CA	LEU	A	167	16.219	6.552	-1.465	1.00	16.11
ATOM	1172	C	LEU	A	167	17.395	6.044	-2.300	1.00	19.87
ATOM	1173	O	LEU	A	167	17.265	4.869	-2.612	1.00	21.38
ATOM	1174	CB	LEU	A	167	15.086	5.624	-1.555	1.00	23.45
ATOM	1175	CG	LEU	A	167	14.123	5.773	-0.401	1.00	33.91
ATOM	1176	CD1	LEU	A	167	12.969	4.908	-0.793	1.00	42.10
ATOM	1177	CD2	LEU	A	167	14.776	5.385	0.903	1.00	25.86
ATOM	1178	N	ILE	A	168	18.534	6.726	-2.507	1.00	21.67
ATOM	1179	CA	ILE	A	168	19.608	6.051	-3.170	1.00	23.38
ATOM	1180	C	ILE	A	168	20.675	5.585	-2.189	1.00	20.47
ATOM	1181	O	ILE	A	168	21.139	6.541	-1.581	1.00	18.08
ATOM	1182	CB	ILE	A	168	20.254	6.835	-4.297	1.00	23.50
ATOM	1183	CG1	ILE	A	168	21.232	7.874	-3.800	1.00	13.71
ATOM	1184	CG2	ILE	A	168	19.445	7.627	-5.276	1.00	18.16
ATOM	1185	CD1	ILE	A	168	20.908	8.938	-4.804	1.00	26.95
ATOM	1186	N	ILE	A	169	21.396	4.478	-2.394	1.00	18.32
ATOM	1187	CA	ILE	A	169	22.554	4.448	-1.536	1.00	13.25
ATOM	1188	C	ILE	A	169	23.924	4.662	-1.967	1.00	11.95
ATOM	1189	O	ILE	A	169	24.615	3.942	-2.539	1.00	20.35
ATOM	1190	CB	ILE	A	169	22.503	3.351	-0.499	1.00	21.07
ATOM	1191	CG1	ILE	A	169	23.398	2.181	-0.655	1.00	11.06
ATOM	1192	CG2	ILE	A	169	21.122	2.801	-0.533	1.00	7.02
ATOM	1193	CD1	ILE	A	169	22.581	1.266	-1.587	1.00	32.83
ATOM	1194	N	THR	A	170	24.570	5.586	-1.296	1.00	17.16
ATOM	1195	CA	THR	A	170	25.883	6.217	-1.397	1.00	13.01
ATOM	1196	C	THR	A	170	26.722	5.719	-0.240	1.00	10.14
ATOM	1197	O	THR	A	170	26.334	5.036	0.758	1.00	9.98
ATOM	1198	CB	THR	A	170	25.623	7.713	-1.344	1.00	15.02
ATOM	1199	OG1	THR	A	170	26.466	7.947	-0.255	1.00	23.39
ATOM	1200	CG2	THR	A	170	24.389	7.914	-0.452	1.00	41.10
ATOM	1201	N	PRO	A	171	28.000	5.738	-0.469	1.00	10.12
ATOM	1202	CA	PRO	A	171	29.012	5.066	0.339	1.00	11.88
ATOM	1203	C	PRO	A	171	28.897	5.492	1.765	1.00	9.74
ATOM	1204	O	PRO	A	171	28.904	4.682	2.646	1.00	9.54
ATOM	1205	CB	PRO	A	171	30.414	5.207	-0.286	1.00	7.15
ATOM	1206	CG	PRO	A	171	30.017	5.603	-1.654	1.00	7.18
ATOM	1207	CD	PRO	A	171	28.667	6.233	-1.601	1.00	6.90
ATOM	1208	N	ALA	A	172	28.725	6.718	1.980	1.00	6.71
ATOM	1209	CA	ALA	A	172	28.247	7.315	3.169	1.00	8.62
ATOM	1210	C	ALA	A	172	27.075	6.631	3.892	1.00	10.99
ATOM	1211	O	ALA	A	172	27.037	6.755	5.165	1.00	16.49
ATOM	1212	CB	ALA	A	172	27.904	8.812	3.040	1.00	2.86
ATOM	1213	N	HIS	A	173	26.287	5.815	3.278	1.00	6.36
ATOM	1214	CA	HIS	A	173	25.133	5.468	4.081	1.00	5.29
ATOM	1215	C	HIS	A	173	25.685	4.314	4.888	1.00	10.58
ATOM	1216	O	HIS	A	173	25.082	3.598	5.668	1.00	9.36

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ATOM	1217	CB	HIS	A	173	24.081	4.883	3.216	1.00	8.41
ATOM	1218	CG	HIS	A	173	22.815	4.403	3.791	1.00	7.30
ATOM	1219	ND1	HIS	A	173	22.066	5.327	4.565	1.00	8.48
ATOM	1220	CD2	HIS	A	173	22.148	3.264	3.670	1.00	7.83
ATOM	1221	CE1	HIS	A	173	20.932	4.657	4.861	1.00	17.36
ATOM	1222	NE2	HIS	A	173	20.945	3.423	4.379	1.00	5.29
ATOM	1223	N	LEU	A	174	26.823	3.947	4.326	1.00	8.03
ATOM	1224	CA	LEU	A	174	27.344	2.623	4.682	1.00	8.06
ATOM	1225	C	LEU	A	174	28.171	2.787	5.930	1.00	13.06
ATOM	1226	O	LEU	A	174	28.609	1.648	6.151	1.00	19.88
ATOM	1227	CB	LEU	A	174	28.078	2.118	3.488	1.00	2.76
ATOM	1228	CG	LEU	A	174	27.560	0.902	2.847	1.00	13.35
ATOM	1229	CD1	LEU	A	174	26.024	1.017	2.796	1.00	18.01
ATOM	1230	CD2	LEU	A	174	27.913	0.740	1.421	1.00	21.70
ATOM	1231	N	SER	A	175	28.290	3.989	6.447	1.00	12.43
ATOM	1232	CA	SER	A	175	29.230	4.052	7.553	1.00	18.01
ATOM	1233	C	SER	A	175	28.872	4.811	8.847	1.00	19.89
ATOM	1234	O	SER	A	175	28.968	6.047	9.120	1.00	14.61
ATOM	1235	CB	SER	A	175	30.516	4.606	6.847	1.00	20.11
ATOM	1236	OG	SER	A	175	30.834	5.907	7.293	1.00	27.73
ATOM	1237	N	TYR	A	176	28.479	3.978	9.815	1.00	17.89
ATOM	1238	CA	TYR	A	176	28.092	4.530	11.133	1.00	12.54
ATOM	1239	C	TYR	A	176	28.530	3.671	12.272	1.00	11.16
ATOM	1240	O	TYR	A	176	27.949	3.770	13.257	1.00	7.63
ATOM	1241	CB	TYR	A	176	26.511	4.283	11.053	1.00	9.13
ATOM	1242	CG	TYR	A	176	25.831	5.525	10.029	1.00	5.03
ATOM	1243	CD1	TYR	A	176	25.874	6.923	10.425	1.00	2.75
ATOM	1244	CD2	TYR	A	176	25.152	5.022	8.980	1.00	2.18
ATOM	1245	CE1	TYR	A	176	25.287	7.754	9.633	1.00	4.25
ATOM	1246	CE2	TYR	A	176	24.649	5.981	8.085	1.00	6.77
ATOM	1247	CZ	TYR	A	176	24.658	7.329	8.399	1.00	6.22
ATOM	1248	OH	TYR	A	176	24.074	8.375	7.635	1.00	5.76
ATOM	1249	N	THR	A	177	29.430	2.685	12.167	1.00	10.72
ATOM	1250	CA	THR	A	177	29.797	1.854	13.284	1.00	13.31
ATOM	1251	C	THR	A	177	30.516	2.659	14.320	1.00	12.46
ATOM	1252	O	THR	A	177	30.311	2.436	15.475	1.00	13.12
ATOM	1253	CB	THR	A	177	30.658	0.683	12.798	1.00	3.49
ATOM	1254	OG1	THR	A	177	31.361	1.247	11.870	1.00	32.08
ATOM	1255	CG2	THR	A	177	29.675	-0.149	12.083	1.00	6.42
ATOM	1256	N	ILE	A	178	31.409	3.474	13.920	1.00	10.48
ATOM	1257	CA	ILE	A	178	32.203	4.246	14.783	1.00	15.25
ATOM	1258	C	ILE	A	178	31.180	5.045	15.632	1.00	16.95
ATOM	1259	O	ILE	A	178	31.092	4.774	16.851	1.00	22.68
ATOM	1260	CB	ILE	A	178	33.338	5.121	14.357	1.00	25.11
ATOM	1261	CG1	ILE	A	178	34.701	4.496	14.056	1.00	25.05
ATOM	1262	CG2	ILE	A	178	33.599	6.205	15.392	1.00	27.60
ATOM	1263	CD1	ILE	A	178	34.553	3.006	14.071	1.00	55.86
ATOM	1264	N	GLU	A	179	30.218	5.799	15.178	1.00	16.34
ATOM	1265	CA	GLU	A	179	29.290	6.610	15.985	1.00	16.94
ATOM	1266	C	GLU	A	179	28.324	5.713	16.692	1.00	14.79
ATOM	1267	O	GLU	A	179	27.683	6.012	17.716	1.00	19.20
ATOM	1268	CB	GLU	A	179	28.555	7.637	15.169	1.00	21.16
ATOM	1269	CG	GLU	A	179	28.790	7.283	13.691	1.00	50.37

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ATOM	1270	CD	GLU	A	179	29.933	7.701	12.851	1.00 61.82
ATOM	1271	OE1	GLU	A	179	30.163	8.890	12.697	1.00 77.56
ATOM	1272	OE2	GLU	A	179	30.627	6.854	12.309	1.00 75.83
ATOM	1273	N	ALA	A	180	28.240	4.418	16.412	1.00 8.00
ATOM	1274	CA	ALA	A	180	27.353	3.520	17.042	1.00 14.34
ATOM	1275	C	ALA	A	180	28.048	2.991	18.280	1.00 19.53
ATOM	1276	O	ALA	A	180	27.397	3.142	19.265	1.00 21.17
ATOM	1277	CB	ALA	A	180	26.843	2.437	16.128	1.00 11.97
ATOM	1278	N	ARG	A	181	29.317	2.547	18.287	1.00 21.89
ATOM	1279	CA	ARG	A	181	29.992	1.982	19.398	1.00 16.48
ATOM	1280	C	ARG	A	181	30.296	3.106	20.367	1.00 19.44
ATOM	1281	O	ARG	A	181	30.243	3.104	21.639	1.00 28.53
ATOM	1282	CB	ARG	A	181	31.310	1.408	19.143	1.00 12.43
ATOM	1283	CG	ARG	A	181	31.954	0.432	20.052	1.00 45.44
ATOM	1284	CD	ARG	A	181	32.596	-0.688	19.242	1.00 66.21
ATOM	1285	NE	ARG	A	181	33.333	-0.030	18.164	1.00 85.83
ATOM	1286	CZ	ARG	A	181	33.306	-0.321	16.895	1.00 91.35
ATOM	1287	NH1	ARG	A	181	32.551	-1.320	16.530	1.00 96.98
ATOM	1288	NH2	ARG	A	181	34.023	0.400	16.095	1.00 92.83
ATOM	1289	N	GLY	A	182	30.387	4.262	19.847	1.00 13.94
ATOM	1290	CA	GLY	A	182	30.553	5.404	20.728	1.00 7.40
ATOM	1291	C	GLY	A	182	29.741	6.574	20.960	1.00 7.95
ATOM	1292	O	GLY	A	182	29.171	6.512	22.083	1.00 12.73
ATOM	1293	N	GLU	A	183	29.725	7.622	20.138	1.00 6.42
ATOM	1294	CA	GLU	A	183	28.816	8.775	20.405	1.00 10.04
ATOM	1295	C	GLU	A	183	27.421	8.369	20.645	1.00 14.41
ATOM	1296	O	GLU	A	183	26.846	8.530	21.749	1.00 15.43
ATOM	1297	CB	GLU	A	183	29.053	9.791	19.402	1.00 21.24
ATOM	1298	CG	GLU	A	183	28.079	10.638	18.725	1.00 62.21
ATOM	1299	CD	GLU	A	183	28.248	12.103	19.141	1.00 81.34
ATOM	1300	OE1	GLU	A	183	28.850	12.243	20.232	1.00 95.85
ATOM	1301	OE2	GLU	A	183	27.791	13.027	18.430	1.00 90.85
ATOM	1302	N	ALA	A	184	26.766	7.605	19.808	1.00 15.56
ATOM	1303	CA	ALA	A	184	25.444	7.083	20.117	1.00 14.54
ATOM	1304	C	ALA	A	184	25.549	6.382	21.464	1.00 13.62
ATOM	1305	O	ALA	A	184	24.575	6.533	22.215	1.00 16.75
ATOM	1306	CB	ALA	A	184	25.019	6.015	19.089	1.00 9.58
ATOM	1307	N	ALA	A	185	26.428	5.396	21.774	1.00 9.42
ATOM	1308	CA	ALA	A	185	26.219	4.677	23.031	1.00 7.48
ATOM	1309	C	ALA	A	185	26.330	5.715	24.100	1.00 12.30
ATOM	1310	O	ALA	A	185	25.761	5.503	25.179	1.00 9.50
ATOM	1311	CB	ALA	A	185	27.138	3.475	23.260	1.00 4.60
ATOM	1312	N	ARG	A	186	27.271	6.673	24.090	1.00 15.54
ATOM	1313	CA	ARG	A	186	27.352	7.507	25.300	1.00 13.57
ATOM	1314	C	ARG	A	186	26.085	8.286	25.561	1.00 11.49
ATOM	1315	O	ARG	A	186	25.421	8.267	26.573	1.00 8.74
ATOM	1316	CB	ARG	A	186	28.484	8.460	25.043	1.00 30.29
ATOM	1317	CG	ARG	A	186	29.869	7.851	25.240	1.00 37.15
ATOM	1318	CD	ARG	A	186	30.983	8.826	24.813	1.00 42.36
ATOM	1319	NE	ARG	A	186	31.902	7.942	24.064	1.00 51.82
ATOM	1320	CZ	ARG	A	186	32.324	8.346	22.870	1.00 50.20
ATOM	1321	NH1	ARG	A	186	31.924	9.538	22.424	1.00 47.65
ATOM	1322	NH2	ARG	A	186	33.115	7.476	22.318	1.00 39.90

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ATOM	1323	N	PHE	A	187	25.565	8.774	24.434	1.00	8.37
ATOM	1324	CA	PHE	A	187	24.195	9.370	24.426	1.00	13.48
ATOM	1325	C	PHE	A	187	23.187	8.476	25.182	1.00	15.92
ATOM	1326	O	PHE	A	187	22.379	8.916	25.995	1.00	14.81
ATOM	1327	CB	PHE	A	187	23.667	9.791	23.087	1.00	11.81
ATOM	1328	CG	PHE	A	187	22.282	10.323	23.032	1.00	14.64
ATOM	1329	CD1	PHE	A	187	21.984	11.586	23.391	1.00	8.47
ATOM	1330	CD2	PHE	A	187	21.186	9.599	22.564	1.00	18.34
ATOM	1331	CE1	PHE	A	187	20.698	12.134	23.353	1.00	12.89
ATOM	1332	CE2	PHE	A	187	19.895	10.026	22.485	1.00	17.42
ATOM	1333	CZ	PHE	A	187	19.661	11.322	22.924	1.00	3.70
ATOM	1334	N	LEU	A	188	23.033	7.232	24.803	1.00	15.17
ATOM	1335	CA	LEU	A	188	21.908	6.427	25.324	1.00	18.43
ATOM	1336	C	LEU	A	188	22.207	6.221	26.775	1.00	19.67
ATOM	1337	O	LEU	A	188	21.280	6.512	27.461	1.00	18.17
ATOM	1338	CB	LEU	A	188	21.703	5.088	24.552	1.00	18.72
ATOM	1339	CG	LEU	A	188	21.116	5.375	23.136	1.00	9.96
ATOM	1340	CD1	LEU	A	188	20.950	4.066	22.601	1.00	7.86
ATOM	1341	CD2	LEU	A	188	19.849	6.206	23.168	1.00	4.70
ATOM	1342	N	ARG	A	189	23.333	5.805	27.230	1.00	17.48
ATOM	1343	CA	ARG	A	189	23.798	5.812	28.547	1.00	18.41
ATOM	1344	C	ARG	A	189	23.353	7.039	29.321	1.00	16.87
ATOM	1345	O	ARG	A	189	22.852	7.164	30.389	1.00	13.64
ATOM	1346	CB	ARG	A	189	25.325	6.017	28.529	1.00	21.93
ATOM	1347	CG	ARG	A	189	25.882	5.624	29.894	1.00	19.95
ATOM	1348	CD	ARG	A	189	27.239	6.140	30.235	1.00	21.42
ATOM	1349	NE	ARG	A	189	27.257	7.545	29.926	1.00	25.62
ATOM	1350	CZ	ARG	A	189	28.491	7.983	29.699	1.00	29.22
ATOM	1351	NH1	ARG	A	189	29.315	6.960	29.840	1.00	26.71
ATOM	1352	NH2	ARG	A	189	28.780	9.210	29.383	1.00	33.27
ATOM	1353	N	ASP	A	190	23.837	8.150	28.796	1.00	13.76
ATOM	1354	CA	ASP	A	190	23.489	9.338	29.615	1.00	17.78
ATOM	1355	C	ASP	A	190	22.008	9.364	29.711	1.00	16.79
ATOM	1356	O	ASP	A	190	21.661	9.891	30.692	1.00	23.13
ATOM	1357	CB	ASP	A	190	23.995	10.663	29.070	1.00	23.17
ATOM	1358	CG	ASP	A	190	25.553	10.664	29.079	1.00	33.40
ATOM	1359	OD1	ASP	A	190	26.250	9.836	29.761	1.00	22.68
ATOM	1360	OD2	ASP	A	190	25.961	11.595	28.321	1.00	30.24
ATOM	1361	N	ARG	A	191	21.156	9.128	28.781	1.00	21.61
ATOM	1362	CA	ARG	A	191	19.707	9.265	28.849	1.00	20.99
ATOM	1363	C	ARG	A	191	19.176	8.237	29.825	1.00	21.23
ATOM	1364	O	ARG	A	191	18.327	8.515	30.651	1.00	20.98
ATOM	1365	CB	ARG	A	191	19.014	9.214	27.450	1.00	19.76
ATOM	1366	CG	ARG	A	191	19.605	10.282	26.521	1.00	27.49
ATOM	1367	CD	ARG	A	191	18.848	11.594	26.689	1.00	36.68
ATOM	1368	NE	ARG	A	191	17.559	11.023	27.144	1.00	60.89
ATOM	1369	CZ	ARG	A	191	16.841	11.651	28.087	1.00	73.30
ATOM	1370	NH1	ARG	A	191	17.404	12.780	28.496	1.00	76.65
ATOM	1371	NH2	ARG	A	191	15.675	11.224	28.574	1.00	62.02
ATOM	1372	N	ILE	A	192	19.734	7.037	29.885	1.00	21.02
ATOM	1373	CA	ILE	A	192	19.500	6.080	30.913	1.00	21.92
ATOM	1374	C	ILE	A	192	19.705	6.598	32.337	1.00	25.67
ATOM	1375	O	ILE	A	192	19.145	6.053	33.263	1.00	27.95

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ATOM   1376  CB  ILE A 192      20.289   4.775  30.750  1.00 21.
ATOM   1377  CG1 ILE A 192      19.770   4.215  29.475  1.00
ATOM   1378  CG2 ILE A 192      19.923   3.983  31.951  1.00
ATOM   1379  CD1 ILE A 192      20.418   2.954  29.019  1.00 21.07
ATOM   1380  N   ARG A 193      20.535   7.574  32.629  1.00 28.72
ATOM   1381  CA  ARG A 193      20.800   8.068  33.963  1.00 33.95
ATOM   1382  C   ARG A 193      20.116   9.377  34.406  1.00 42.87
ATOM   1383  O   ARG A 193      20.479   9.267  35.618  1.00 48.19
ATOM   1384  CB  ARG A 193      22.298   8.179  34.167  1.00 34.19
ATOM   1385  CG  ARG A 193      23.096   6.896  34.100  1.00 39.38
ATOM   1386  CD  ARG A 193      24.590   7.213  34.133  1.00 65.92
ATOM   1387  NE  ARG A 193      25.339   5.973  34.003  1.00 81.05
ATOM   1388  CZ  ARG A 193      26.631   5.765  33.770  1.00 81.52
ATOM   1389  NH1 ARG A 193      27.441   6.816  33.647  1.00 80.92
ATOM   1390  NH2 ARG A 193      27.120   4.536  33.652  1.00 74.00
ATOM   1391  OT  ARG A 193      19.292  10.277  34.082  1.00 38.80
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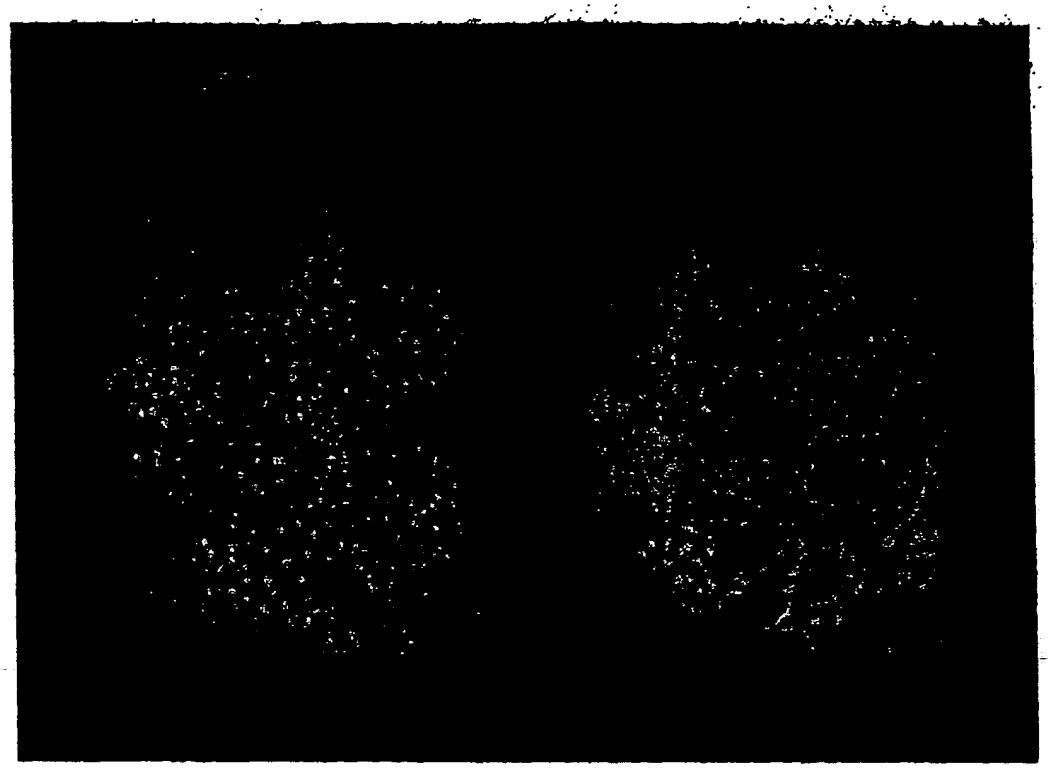

Fig. 2

3D structure of cutinases from *F. solani pisi* (left) and *H. insolens* (right)

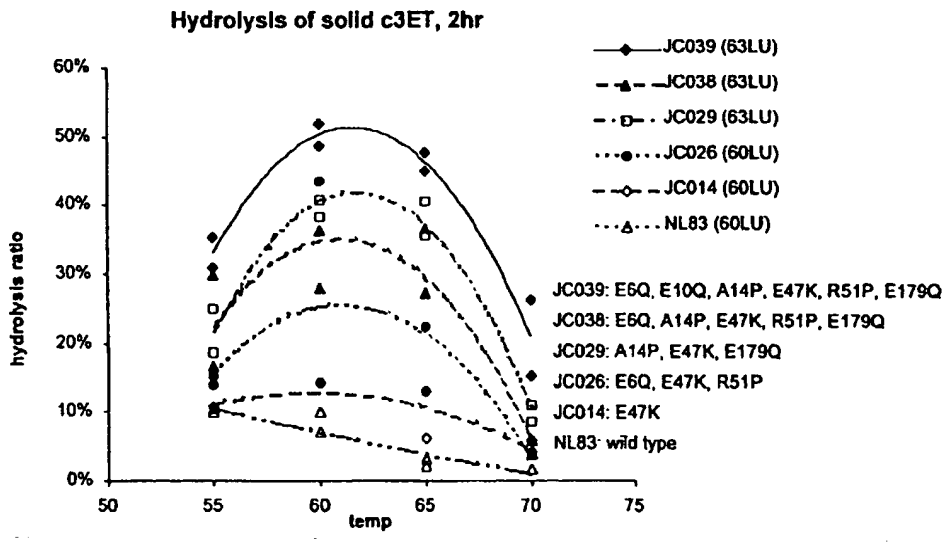

Fig. 3

Hydrolysis of solid c3ET, 2 hr

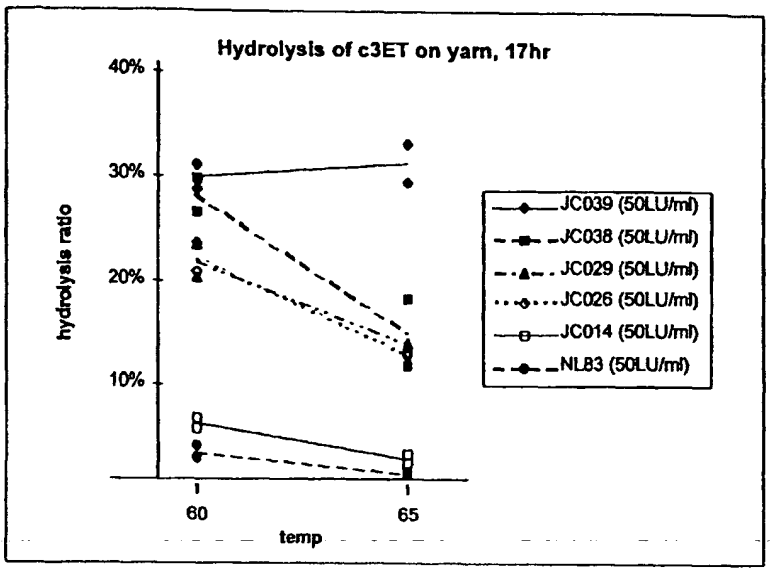

Fig. 4

Hydrolysis of c3ET on yarn, 17 hr

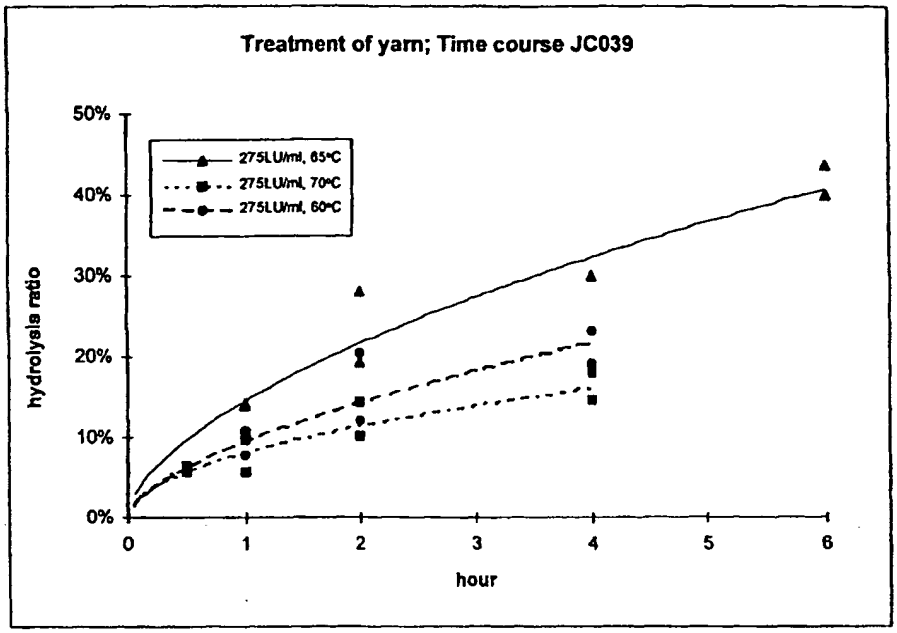

Fig. 5

Treatment of yarn; time course for JC039

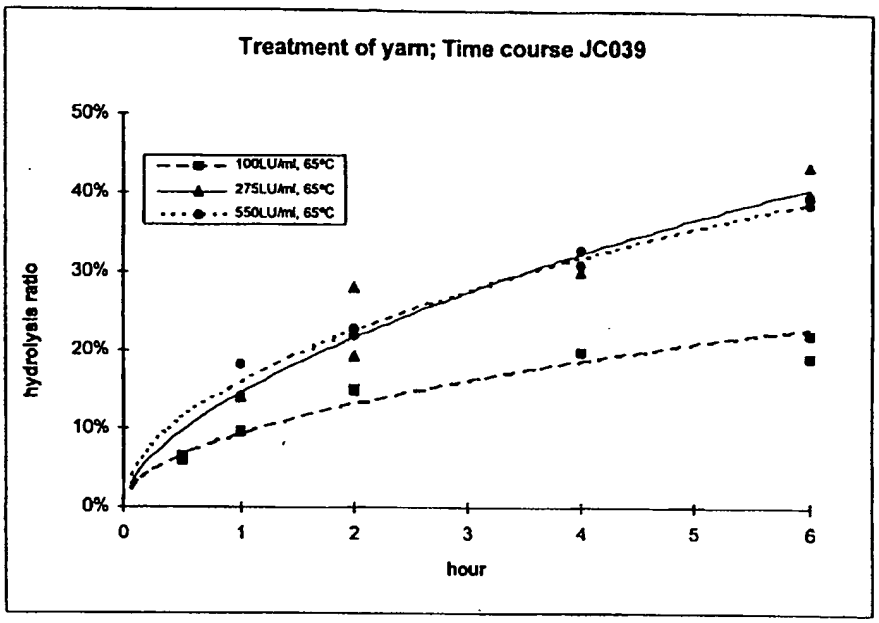

Fig. 6

Treatment of yarn; time course for JC039

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